

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 6, 2004, 15:55:09 ; Search time 194 Seconds
 (without alignments)

625.794 Million cell updates/sec

Title: US-09-633-200-7

Perfect score: 1103

Sequence: 1 MASGGPGPPRQECEPALP.....LWVLSVVLGQFVYRRFFKS 211

Scoring table: BLOSUM62

Gebop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

Database : UniProt 02.*

1: uniprot_sprot;*

2: uniprot_trembl;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1103	100.0	211	1 BAK_HUMAN	Q16611 homo sapien
2	1103	100.0	211	2 CAG33700	Q333700 homo sapien
3	1075	97.5	211	1 BAK2_HUMAN	Q13014 homo sapien
4	977.5	88.6	190	2 Q8NPF3	Q8NPF3 homo sapien
5	845	76.6	209	2 Q8BE64	Q8BE64 mus musculus
6	839	76.1	209	2 Q9JTK59	Q9JTK59 rattus norvegicus
7	829.5	75.2	208	1 BAK_MOUSE	Q93734 mus musculus
8	733	66.5	163	2 Q9MZS5	Q9MZS5 ovis aries
9	452	41.0	151	2 Q91WX5	Q91WX5 mus musculus
10	452	41.0	151	2 AAH57589	AAH57589 mus musculus
11	390	35.4	207	2 Q7738	Q7738 sus scrofa
12	189	17.1	239	1 BCL2_HUMAN	P19415 homo sapiens
13	186	16.9	229	1 BCL2_BOVIN	P07718 bos taurus
14	184	16.7	229	1 BCLX_CHICK	Q07816 gallus gallus
15	183.5	16.6	233	1 BCL2_CHICK	Q09611 gallus gallus
16	181	16.4	211	2 Q9W6F1	Q9W6F1 mus musculus
17	181	16.4	217	2 Q9HN35	Q9HN35 mus musculus
18	181	16.4	233	1 BCLX_MOUSE	Q56373 mus musculus
19	181	16.4	233	1 BCLX RAT	P5563 rattus norvegicus
20	181	16.4	233	2 Q9MYW4	Q9MYW4 oryctolagus cuniculus
21	180.5	16.4	199	2 Q8C5P0	Q8C5P0 mus musculus
22	180	16.3	201	2 Q6GL15	Q6GL15 xenopus tropicalis
23	180	16.3	233	1 BCLX_HUMAN	Q07817 homo sapiens
24	180	16.3	233	2 Q76LT7	Q76LT7 canis familiaris
25	180	16.3	233	2 Q9MZS7	Q9MZS7 ovis aries
26	180	16.3	233	2 Q8SO42	Q8SO42 felis silvestris
27	180	16.3	233	2 BAB71819	BAB71819 canis familiaris
28	180	16.3	233	2 AAP35872	AAP35872 homo sapiens
29	180	16.3	239	2 Q75SV7	Q75SV7 canis familiaris
30	180	16.3	239	2 BAD05044	BAD05044 canis familiaris
31	179.5	16.3	236	1 ECL2_MOUSE	P10417 mus musculus

SEQUENCE FROM N.A. AND VARIANTS VAL-28 AND ARG-69.

SEQUENCE FROM N.A.

ALIGNMENTS

	32	178.5	16.2	236	1 BCL2 RAT
	33	177.5	16.1	236	2 QTTSN8
	34	177.5	16.1	236	2 QBbIK4
	35	177.5	16.1	236	2 Q923R6
	36	177	16.0	233	2 Q9N1A2
	37	176.5	16.0	199	2 Q6NTTH7
	38	176.5	16.0	199	2 AAH6888
	39	176	16.0	180	2 Q9BD5
	40	176	16.0	193	1 BCLW_HUMAN
	41	176	16.0	233	1 BCLX_TIG
	42	175	15.9	235	2 Q81008
	43	174	15.8	180	2 Q9BDX7
	44	173.5	15.7	236	2 Q6R755
	45	173.5	15.7	236	2 AAR92491

- RA Barlow K.F., Bates K., Beare D.M., Beasley H., Beasley O., Bird C.P., RA Eberstadt M., Yoon H.S., Shuker S.B., Chang B.S., Minn A.J., Thompson C.B., Pasik S.W., RT "Structure of Bcl-xL-Bak peptide complex: recognition between regulators of apoptosis." RT Science 275:983-986(1997); RL
- RA Blakey S.E., Bray-Allen S., Brook J., Brown A.J., Brown J.Y., RA RT
- RA Burford D.C., Burilli W., Burton J., Carter C., Carter N.P., RT
- RA Chapman J.C., Clark G., Clegg S., Cobley V., RT
- RA Collier R.E., Collins J.E., Colman L.K., Corry N.R., Coville G.J., RT
- RA Culley K.M., Dhani P., Davies J., Dunn M., Earthrow M.E., CC -I- FUNCTION: In the presence of an appropriate stimulus, accelerates cell death by binding to, and antagonizing the a-CC
- RA Ellington A.E., Evans K.A., Faulkner L., Francis M.D., Frankish A., CC -I- repressor Bcl-2 or its adenovirus homolog E1B 19k protein.
- RA Franklin J., French L., Garner P., Garnett J., Ghori M.J., RT
- RA Gilby L.M., Gillison C.J., Glithero R.J., Graham D.V., Grant M., RT
- RA Gibble S., Griffiths C., Griffiths M.N.D., Hall R., Halls K.S., RT
- RA Hammond S., Harley J.L., Hart B.A., Heath P.D., Heathcott R., RT
- RA Holmes S.J., Howell P.J., Howe K.L., Howell G.R., Huckle E., RT
- RA Humphrey S.J., Humphries M.D., Hunt A.R., Johnson C.M., Joy A.A., RT
- RA Kay M., Keenan S.J., Kimberley A.M., King A., Laird G.K., Langford C., RT
- RA Gilby L.M., Gillison C.J., Glithero R.J., Graham D.V., Grant M., RT
- RA Lawlor D.A., Lechner D.A., Leversha M., Lloyd C.R., Lloyd D.M., RT
- RA Loveland J.E., Lovell J., Martin S., Mashreghi-Mohammadi M., RT
- RA Maslen G.L., Matthews L., McCaughan O.T., McLaren S.J., McLay K., RT
- RA McMurtry M.J.F., Mulliken J.C., Niblett D., Nickerson T., RT
- RA Novik K.L., Oliver K., Overton-Larty E.K., Parker A., Patel R., RT
- RA Pearce A.V., Peck A.I., Phillinore B.J.C.T., Phillips S., Plumb R.W., RT
- RA Porter K.M., Ranney Y., Ranby S.A., Rice C.M., Ross M.T., Searle S.M., RT
- RA Sehra H.K., Sheridan E., Skuce C.D., Smith S., Smith M., Spraggan L., RT
- RA Squares S.L., Steward C.A., Sycamore N., Tamlyn-Hall G., Tester J., RT
- RA Tewell A.J., Thomas D.W., Thorpe A., Tracey A., Tromans A., Tubby B., RT
- RA Wall M., Wallis J.M., West A.P., White S.S., Whithead S.L., RT
- RA Whittaker H., Wild A., Willey D.J., Wimer T.E., Wood J.M., Wray P.W., RT
- RA Wyatt J.C., Young L.L., Yousler R.M., Bentley D.R., Coulson A., RT
- RA Durbin R., Hubbard T., Sulston J.E., Dunham I., Rogers J., Beck S.; RT
- RT "The DNA sequence and analysis of human chromosome 6." RT
- RN Nature 425:805-811(2003). RT
- [6] RN SEQUENCE FROM N.A. RT
- RP TISSUE-LUNG. RT
- RC MEDLINE=22188257; PubMed=12477932; DOI=10.1073/pnas.242603999; RT
- RC TISSUE-LUNG. RT
- RC MEDLINE=22188257; PubMed=12477932; DOI=10.1073/pnas.242603999; RT
- RC TISSUE-LUNG. RT
- RA Feingold E.A., Grouse J.G., Derge J.G., RT
- RA Klausberg R.D., Collins F.S., Wagner L., Sheiner C.M., Schuller G.D., RT
- RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhattacharyya N.K., RT
- RA Hopkins R.F., Jordan R., Moore T., Max S.I., Wang J.Y., Hsieh F., RT
- RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., RT
- RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., RT
- RA Raha S.S., Loquellano N.B., Ustun T.B., Yoshiyuki S., Carnison R.D., Prange C., RT
- RA Bosak S.A., McEvans P.J., McKernan K.J., Malek J.A., Mullahay S.J., RT
- RA Richards S., Worley K.C., Gay L.S., Garcia A.M., Gunaratne P.H., RT
- RA Villalona D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., RT
- RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., RT
- RA Whiting M., Madan A., Young A.C., Bouffard G.G., RT
- RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., RT
- RA Rodriguez A.C., Grimwood J., Schmarz J., Myers R. M., RT
- RA Butterfield Y.S.N., Krywinski M.I., Skalska U., Smailus D.E., RT
- RA Schnieke A., Schein J.E., Jones S.J.M., Marra M.A.; RT
- RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences." RT
- Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002). RT
- RL SEQUENCE OF 96-206 FROM N.A. RT
- RP EGuchi H., Hayashi S.; RT
- RT "Estrogen alters expression of apoptosis-regulators, Bcl-2, Bcl-xL and Bak, as well as susceptibility to therapeutic agents of human breast cancer cells"; RT
- RT submitted (NOV-1996) to the EMBL/GenBank/DBJ databases. RT
- RN SEQUENCES OF Bcl-2, Bcl-xL AND BAK DOMAINS. RT
- RP MUTAGENESIS, AND FUNCTION OF BH3 DOMAIN. RT
- RX MEDLINE=96091131; PubMed=952116; RT
- RA Chittenden T., Flemington C., Houghton A.B., Ebb R.G., Gallo G.J., RT
- RA Elangovan B., Chinnadurai G., Lutz R.J.; RT
- RT "A conserved domain in Bak, distinct from BH1 and BH2, mediates cell death and protein binding functions." RT
- RL BMB0 J. 14:5589-5596(1995). RT
- [9] RN STRUCTURE BY NMR OF 72-87. RT
- RP MEDLINE=97172562; PubMed=2020082; RT
- RX Sattler M., Liang H., Nestesheim D., Meadows R.P., Harlan J.E., RT

Db 61 VTLPLQSSPMQVGRQLAIIIGDDINRYDSEFTMLQHLOPAAENAEYFTKIAATSLFE 120
 QY 121 SGINWGRVALLGCGYRALHYOGLTGLQVTRFYDDEMLHCTARWIAQORGGVAA 180
 Db 121 SGINWGRVALLGCGYRALHYOGLTGLQVTRFYDDEMLHCTARWIAQORGGVAA 180
 QY 181 LNLGNGPILNVLVLYLGVVLLGQFVYRFFKS 211
 Db 181 LNLGNGPILNVLVLYLGVVLLGQFVYRFFKS 211

RESULT 2
 ID CAG33700 PRELIMINARY; PRT; 211 AA.
 AC CAG33700;
 DT 01-JUN-2004 (TREMBurel_27, Created)
 DT 01-JUN-2004 (TREMBurel_27, Last sequence update)
 DT 01-JUN-2004 (TREMBurel_27, Last annotation update)
 DE BAK1 protein.
 GN Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ebert L., Schick M., Neubert P., Schattner R., Henze S., Korn B.;
 RT "Cloning of human full open reading frames in Gateway(TM) system entry
 vector (PDONR201)." ;
 RL Submitted (JUN 2004) to the EMBL/GenBank/DDBJ databases.
 DR EMBL: CR457419; CA633700.1;
 DR SEQ 211 AA; 23409 MW; A2200F72A14D04E CRC44;
 SQ

Query Match 100.0%; Score 1103; DB 2; Length 211;
 Best Local Similarity 100.0%; Pred. No. 4..4..9;
 Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASGGPQPQQCEGPALPSASEQVADTEEVERSXYEYRHQEQPAEGYAAAPADM 60
 Db 1 MASGGPQPQQCEGPALPSASEQVADTEEVERSXYEYRHQEQPAEGYAAAPADM 60
 QY 61 VTLPLQSSPMQVGRQLAIIIGDDINRYDSEFTMLQHLOPAAENAEYFTKIAATSLFE 120
 Db 61 VTLPLQSSPMQVGRQLAIIIGDDINRYDSEFTMLQHLOPAAENAEYFTKIAATSLFE 120
 QY 121 SGINWGRVALLGCGYRALHYOGLTGLQVTRFYDDEMLHCTARWIAQORGGVAA 180
 Db 121 SGINWGRVALLGCGYRALHYOGLTGLQVTRFYDDEMLHCTARWIAQORGGVAA 180
 QY 181 LNLGNGPILNVLVLYLGVVLLGQFVYRFFKS 211
 Db 181 LNLGNGPILNVLVLYLGVVLLGQFVYRFFKS 211

RESULT 3
 BAK2_HUMAN STANDARD; PRT; 211 AA.
 ID BAK2_HUMAN STANDARD;
 AC Q13QT4;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 44, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Putative Bcl-2 homologous antagonist/killer 2 (Apoptosis regulator
 BAK-2)
 GN Name-BCL2L7P1; Synonyms-BAK2;
 OS Homo sapiens (Human).
 OC Mammalia; Eutheria; Primates; Catarrhini; Vertebrata; Buteleostomi;
 OX NCBI_TaxID=9606;
 RN SEQUENCE FROM N.A.
 RP MEDLINE=9523:654; PubMed=7715731;
 RX Kiefer M.C., Brauer M.J., Powers V.C., Wu J.J., Umansky S.R.,
 RA Tomei L.D., Barr P.J.;

RT Modulation of apoptosis by the widely distributed Bcl-2 homologue
 RT Bak.";
 RL Nature 374:736-739(1995).
 CC -!- FUNCTION: In the presence of an appropriate stimulus, accelerates
 programmed cell death by binding to, and antagonizing the a
 repressor Bcl-2 or its adenovirus homolog E1B 19k protein.
 CC -!- SUBUNIT: Forms heterodimers with Bcl-2, E1B 19k Protein, and Bcl-
 CC X(1).
 CC -!- SUBCELLULAR LOCATION: Membrane-associated (Potential).
 CC -!- TISSUE SPECIFICITY: Expressed in a wide variety of tissues, with
 highest levels in the heart and skeletal muscle.
 CC -!- DOMAIN: Intact BH3 domain is required by BIK, BID, BAK, BAD and
 BAX for their pro-apoptotic activity and for their interaction
 with anti-apoptotic members of the Bcl-2 family. Apoptotic members
 CC of the Bcl-2 family.
 CC -!- SIMILARITY: Belongs to the Bcl-2 family.
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
 CC -!- CAUTION: This is Probably the Product of a Pseudogene.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use by non-profit institutions as long as its content is in no way
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 CC or send an email to license@isb-sib.ch).
 CC
 DR PIR: U16812; AAA74467.1; -.
 DR PIR: S58875; S88875.
 DR HSSP: Q1661; S88875.
 DR Genew; HGNC:996; BCL2L7P1.
 DR GO: GO:0016020; C:membrane; NAS.
 DR GO: GO:0008917; P:induction of apoptosis; NAS.
 DR InterPro: IPR006712; Bcl2_BH.
 DR InterPro: IPR002475; BCL2_Family.
 DR Pfam: PF00452; BCL1_1.
 DR SMART: SM00337; BCL1_1.
 DR PS50012; BCL2_FAMILY; 1.
 DR PROSITE: PS001030; BH1_1.
 DR PROSITE: PS01258; BH2_1.
 DR PROSITE; PS01259; BH3_1.
 KW ADPOPTOSIS; Hypothetical protein; Transmembrane.
 FT DOMAIN 74 88 BH3.
 FT DOMAIN 117 136 BH1.
 FT DOMAIN 159 184 BH2.
 FT TRANSMEM 188 205 Potential.
 SQ SEQUENCE 211 AA; 23411 MW; 703875EC4DCC1D3 CRC64;
 Query Match 97.5%; Score 1075; DB 1; Length 211;
 Best Local Similarity 97.2%; Pred. No. 1..4..8;
 Matches 205; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MASGGPQPQQCEGPALPSASEQVADTEEVERSXYEYRHQEQPAEGYAAAPADM 60
 Db 1 MASGGPQPQQCEGPALPSASEQVADTEEVERSXYEYRHQEQPAEGYAAAPADM 60
 Qy 61 VTLPLQSSPMQVGRQLAIIIGDDINRYDSEFTMLQHLOPAAENAEYFTKIAATSLFE 120
 Db 61 VTLPLQSSPMQVGRQLAIIIGDDINRYDSEFTMLQHLOPAAENAEYFTKIAATSLFE 120
 Qy 121 SGINWGRVALLGCGYRALHYOGLTGLQVTRFYDDEMLHCTARWIAQORGGVAA 180
 Db 121 SGINWGRVALLGCGYRALHYOGLTGLQVTRFYDDEMLHCTARWIAQORGGVAA 180
 Qy 181 LNLGNGPILNVLVLYLGVVLLGQFVYRFFKS 211
 Db 181 LNLGNGPILNVLVLYLGVVLLGQFVYRFFKS 211

RESULT 4
 Q8NFF3

ID	Q8NFP3	PRELIMINARY;	PRT;	190 AA.
AC	Q8NFP3;			
DT	01-OCT-2002	(TREMBLrel. 22; Created)		
DT	01-OCT-2002	(TREMBLrel. 22; Last sequence update)		
DT	01-JUN-2003	(TREMBLrel. 24; Last annotation update)		
DE	Pro-apoptotic protein BAXM variant.			
GN	Name=Bak;			
OS	Homo sapiens (Human); Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
OC				
OC				
OX	NCBI_TaxID=9606;			
[1]	RN	SEQUENCE FROM N.A.		
RA	Ma J.;			
RL	Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.			
DR	EMBL; AF520590; AAM74349.1; -.			
DR	HSSP; Q16611; 1BXL.			
DR	GO; GO-004281; P:regulation of apoptosis; IEA.			
DR	InterPro; IPR000712; BCL2_BH.			
DR	InterPro; IPR002475; BCL2_Family.			
DR	PFam; PF00457; Bcl-2_1.			
DR	SMART; SM00337; BCL1.			
DR	PROSITE; PS50062; BCL2_FAMILY; 1.			
DR	PROSITE; PS01080; BH1_1.			
DR	PROSITE; PS01258; BH2_1.			
DR	PROSITE; PS0059; BH3_1.			
SQ	SEQUENCE 190 AA; 21231 MW; A9D4EB8526D0897B CRC64;			
Query	Match 88.6%; Score 977.5; Db 2;			
Best Local Similarity 90.0%; Pred No. 5.9e-79; Gaps 1;	Matches 190; Conservative 0; Mismatches 0; Indels 21;			
Db	1 MASGQQGPGRPPRQSGCPEALPSASSEVQAVQAQDTTEEVFRSYFVYRHQQEQBAEGVAAPADPEM 60			
Qy	1 MASGQQGPGRPPRQSGCPEALPSASSEVQAVQAQDTTEEVFRSYFVYRHQ-----44			
Db	61 VTIPLQPQSTMGQVGRQALIGDINRRDSEQTMLQLQPTAAENAEYFTKTAISLFB 120			
Qy	45 -----OPSSSTMGVGRQLAIIIGDINRRDSEQTMLQLQPTAAENAEYFTKTAISLFB 99			
Db	121 SGINWGRVVALIIGGRYLAHYQGLTQFLGQVTRFYVDFMLHICARWIQORGWYAA 180			
Qy	100 SGINWGRVVALIIGGRYLAHYQGLTQFLGQVTRFYVDFMLHICARWIQORGWYAA 159			
Db	181 LNIGNGPILINVLVYLGVVLLGQFVVRFFKS 211			
Qy	160 LNIGNGPILINVLVYLGVVLLGQFVVRFFKS 190			
RESULT 5				
Q8C264	PRELIMINARY;	PRT;	209 AA.	
ID	Q8C264			
AC	Q8C264;			
DT	01-MAR-2003	(TREMBLrel. 23; Created)		
DT	01-MAR-2003	(TREMBLrel. 23; Last sequence update)		
DT	01-MAR-2004	(TREMBLrel. 26; Last annotation update)		
DB	Mus musculus NOD-derived cDNA +ve dendritic cells cDNA, RIKEN full-length enriched library, clone:630041U23 product:BC12-antagonist/killer 1, full insert sequence.			
DE	Name=Bak1;			
GN	Mus musculus (Mouse).			
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
OC				
OC				
NCBI_TaxID=10090;				
RN	SEQUENCE FROM N.A.			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=NOD;			
RX	Medline=992925; PubMed=10349636;			
RA	Carnici U; Hayashizaki Y;			
RT	"High-efficiency full-length cDNA cloning."			
RL	Meth. Enzymol. 303:19-44 (1999).			
RP	SEQUENCE FROM N.A.			

Db	59	DNISLEPNSVLGQVQLALIGDDINRRDTEFQNLLEQQPTAGNAYELFTKASSLFLK	118
Qy	121	SGINNGRVALLGFGYRLAHVYQHGLTGFQTVYDFMLHICIAWIAQRGWVAA	180
Db	119	SGINNGRVALLGFGYRLAHVYQHGLTGFQTVYDFMLHICIAWIAQRGWVAA	178
Qy	181	LNLGNGPILNVLGVVLLGVVLLQFVYVRFPKS	211
Db	179	LNLRRDPILTVVIFGVVLLGQFVYVRFPKS	209
RESULT 6			
	Q9JK59	PRELIMINARY;	PRT; 209 AA.
	ID Q9JK59;		
	AC Q9JK59;		
	DT 01-OCT-2000 (TREMBLrel. 15, Created)		
	DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)		
	DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)		
	DE BAK protein.		
	GN Name=Bak;		
	OS Rattus norvegicus (Rat).		
	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteostomi;		
	OC Mammalia; Eutheria; Rodentia; Sciurogнатhi; Muridae; Rattus.		
	OC NCBI_TaxID=10116;		
	RN [1]		
	RP SEQUENCE FROM N.A.		
	RC STRAIN=Sprague-Dawley;		
	RX MEDLINS=22672518; PubMed=12787069,		
	RA Itoh T, Itch A, Pleasure D.;		
	RT "Bcl-2-related protein family gene expression during oligodendroglial differentiation."		
	RL J Neurochem. 85:1500-1512(2003).		
	DR AF295054; ARF71760.1; HSSP: Q16611; IBXL.		
	GO: GO:0042981; P: regulation of apoptosis; EA.		
	DR IntertPro; IPR000712; BCL2_BI.		
	DR IntertPro; IPR002475; BCL2_BI.		
	PFam: PF004432; BCL-2_1.		
	DR SMART: SM00337; BCL-2_1.		
	DR PROSITE: PS50162; BCL2_FAMILY; 1.		
	DR PROSITE: PS00180; BH1; UNKNOWN_1.		
	DR PROSITE: PS01259; BH2; 1.		
	DR PROSITE: PS01258; BH3; 1.		
	SQ SEQUENCE 209 AA; 23153 MW; 2493B814B1972421-CRC64;		
Query Match	76.1%	Score 839; DB 2; Length 209;	
Best Local Similarity	77.3%	Pred. No. 1.5e-66;	
Matches	163;	Conservative 23; Mismatches 23; Indels 2; Gaps 2;	
Qy	1	MASGQGPQPGPQQECPGEALPSASEQVAQDTEEVFRSYFYRHOQEAEQVAAPADPEM	60
Db	1	MASGQGPQPGKGDDE-AI-SASSEQVQAQDTEEVFRSYFYLHQEQETQGAATANPEN	58
Qy	61	VTLPLQPSSTMGQVQLALIGDDINRRDSEFQTMQHQOPTAENAYEFYTKATSLFE	120
Db	59	DNISLEPNSVLGQVQLALIGDDINRRDTEFQNLLEQQPTAGNAYELFTKASSLFLK	118
Qy	121	SGINNGRVALLGFGYRLAHVYQHGLTGFQTVYDFMLHICIAWIAQRGWVAA	180
Db	119	SGINNGRVALLGFGYRLAHVYQHGLTGFQTVYDFMLHICIAWIAQRGWVAA	178
Qy	181	LNLGNGPILNVLGVVLLGVVLLQFVYVRFPKS	211
Db	179	LNLRRDPILSVVVIFGVVLLGQFVYVRFPKS	209
RESULT 7			
	BAK_MOUSE	STANDARD;	PRT; 208 AA.
	AC C08734;		
	DT 01-NOV-1997 (Rel. 35, Created)		
	DT 01-NOV-1997 (Rel. 35, Last sequence update)		

RT	Neuron-specific BCI-2 homology 3 domain-only splice variant Crxex. ¹⁴			
RL	anti-apoptotic in neurons, but pro-apoptotic in non-neuronal cells. ¹⁵			
RN	J. Biol. Chem. 276:16240-16247 (2001).			
RP				
	SEQUENCE FROM N.A.			
RC	STRAIN=57BL/6; TISSUE=Brain;			
RX	MEDLINE=22388257; PubMed=12477932;			
RA	Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shaeffer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F., Diatchenko L., Marusita K., Farmer A.A., Rubin G.M., Hogen E., Sharpless M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., McEwan P.J., McKernan K.J., Mullahy S.J., Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Gunnarsson P.H., Bosak S.A., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.Z., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Farley J., Heitton B., Kettenm M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez R.W., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smilis D.E., Schinrich A., Schein J.E., Jones S.J., Marras M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).			
RA	SEQUENCE FROM N.A.			
RC	STRAIN=57BL/6; TISSUE=Brain;			
RX	Strausberg R.; Submitted (SSP-2003) to the EMBL/GenBank/DDBJ databases.			
RA	EMBL: AF402617; AAL0176.1; -;			
DR	BC057389; AAH57389.1; -;			
DR	HSSP; Q16111; 1BXL;			
DR	MGI:1097161; Bak1.			
GO	GO:0008335; P: caspase activation via cytochrome c; IMP.			
RA	InterPro; IPR00712; Bcl2_BH.			
DR	InterPro; IPR002415; BCL2_FAMILY.			
DR	PFAM; PF00412; Bcl-2; 1.			
DR	PROSITE; PS0062; BCL2_FAMILY; 1.			
DR	PROSITE; PS0159; BH3_1.			
SQ	SEQUENCE 151 AA; 1640 MW; 18C13BFF86B4F33B CRC64;			
Query Match	41.0% ; Score 452; DB 2; Length 151;			
Best Local Similarity	75.0% ; Pred. No. 3e-32; 1;			
Matches	Conservative 12; Mismatches 15; Indels 2; Gaps 1;			
Qy	1 MASQQGPGRQBGEPALPSASEEQQAQDTTERFSYFYRHQQEQAEGYAAPADEM 60			
Db	1 MASCGQGPGRPKVQCDSE--PSPESEQVAQDTEEVRSYFYHLQQEQTQGAAPANPEM 58			
Qy	61 VTLPLQPSSTMTGQVGRQLAIIGDDINRKYRDSEQTMLQHLPQTAENAYEFKIA 116			
Db	59 DNLEPNLSILGVGRQLALIGDDINRKYDTEQNLLEQLQPTAGNAYELFTKIAS 114			
	RESULT 10			
	AAH57589 PRELIMINARY; PRT; 151 AA.			
[1]	AAH57589 PRELIMINARY; PRT; 151 AA.			
AC	AAH57589 PRELIMINARY; PRT; 151 AA.			
DT	02-MAR-2004 (TREMBLre). 27, Created)			
DT	02-MAR-2004 (TREMBLre). 27, Last sequence update)			
DE	Bak1 protein			
OS	Mus musculus (Mouse)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10030; NCBI_TaxID=10030;			
RN	SEQUENCE FROM N.A.			
STRAIN=NMM-Na; TISSUE=Neuronal; MEDLINE=21238300; PubMed=11278671; Sun Y.P., Yu L.Y., Saarma M., Timmusk T., Arumae U.,				
RP	SEQUENCE FROM N.A.			
RC	STRAIN=57BL/6; TISSUE=Brain; MEDLINE=22388257; PubMed=12477932;			
RX				

RA	Straubinger R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Derge J.G., Schuler G.D., Altenschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.R., Diatchenko L., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Stapleton M., Soares M.B., Bonaldo M.F., Cesavant T.L., Scheetz T.B., Brownstein M.J., Usain T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquaiato N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek R., Gunaratne P.H.J., Richards S., Worley K.C., Garcia S., Hale S., Garcia A.M., Hulyk S.W., Villalon D.K., Muzyk D.M., Soderberg E.J., Lu X., Gibbs R.A.; Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smalius D.E., Schnurch A., Schein J.E., Jones S.J., Matra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).	Qy	50 EGVAAPADPEWTLPLQPSSTMQVGRQLAIGDINRYDSEFFTMQLHQIQLQPTAENAYE 109 1 DGAAPAPDPEWTLPLEPSTMQVGRQLAIGDINRYDSEFFTMQLHQIQLQPTAENAYE 60
RA	BCL2_HUMAN STANDARD; ID: BCL2_HUMAN; STANDARD; PRT; 239 AA.	Db	1 YFTKIAATSLFESGINGRVV 129 1 YFTKIAATSLFESGINGRVV 80
RA	AC: P10415; Q13842; Q16197;	Qy	110 YFTKIAATSLFESGINGRVV 129
RA	DT: 01-MAR-1989 (Rel. 10, Created)	Db	61 YFTKIAATSLFESGINGRVV 80
RA	DT: 01-OCT-2004 (Rel. 45, Last sequence update)	DE	Apoptosis regulator Bcl-2.
RA	DE: Adoptosis regulator Bcl-2.	GN	Name=BCL2;
RA	OS: Homo sapiens (Human)	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
RA	OC: Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.	OX	NCB_Taxid:9606;
RA	RN: SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).	RN	SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
RA	RX: MEDLINE=86259760; PubMed=3523487;	RX	MEDLINE=92375724; PubMed=1508712.
RA	RA: Tsujimoto Y., Croce C.M.; "Analysis of the structure, transcripts, and protein products of bcl-2, the gene involved in human follicular lymphoma."; Proc. Natl. Acad. Sci. U.S.A. 83:5214-5218 (1986).	RA	RA: Tsujimoto Y., Ewer D.L., Tsujimoto Y.; "Isolation and characterization of the chicken bcl-2 gene: expression in a variety of tissues including lymphoid and neuronal organs in adult and embryo."; Nucleic Acids Res. 20:4187-4192 (1992).
RA	RL: REVISIONS TO 96; 110 AND 237.	RL	RL: REVISIONS TO 96; 110 AND 237.
RA	RX: MEDLINE=92375724; PubMed=1508712.	RX	RX: MEDLINE=92375724; PubMed=1508712.
RA	RA: Cleary M.L., Smith S.D., Sklar J.; "Cloning and structural analysis of cDNAs for bcl-2 and a hybrid bcl-2/immunoglobulin transcript resulting from the t(14;18) translocation"; Cell 47:19-28 (1986).	RA	RA: Cleary M.L., Smith S.D., Sklar J.; "Cloning and structural analysis of cDNAs for bcl-2 and a hybrid bcl-2/immunoglobulin transcript resulting from the t(14;18) translocation"; Cell 47:19-28 (1986).
RA	RN: SEQUENCE FROM N.A. (ISOFORM ALPHA).	RN	SEQUENCE FROM N.A. (ISOFORM ALPHA).
RA	RX: MEDLINE=88196701; PubMed=2834197;	RX	SEQUENCE FROM N.A. (ISOFORM ALPHA).
RA	RA: Seto M., Jaeger U., Hockett R.D., Graninger W., Bennett S., Goldan P., Korsmeyer S.J.; "Alternative promoters and exons, somatic mutation and deregulation of the Bcl-2-19 fusion gene in lymphoma."; EMBO J. 7:1123-1131 (1988).	RA	RA: Seto M., Jaeger U., Hockett R.D., Graninger W., Bennett S., Goldan P., Korsmeyer S.J.; "Alternative promoters and exons, somatic mutation and deregulation of the Bcl-2-19 fusion gene in lymphoma."; EMBO J. 7:1123-1131 (1988).
RA	RN: SEQUENCE FROM N.A. (ISOFORM ALPHA).	RN	SEQUENCE FROM N.A. (ISOFORM ALPHA).
RA	RX: MEDLINE=12388157; PubMed=12477932; DOI=10.1073/pnas.242603899;	RX	SEQUENCE FROM N.A. (ISOFORM ALPHA), AND VARIANT THR-43.
RA	RX: Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Riede M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung M.-W., Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D., Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D., Schatzkowitz W.S., Sherwood J.K., Wittrak L.A., Nickerson D.A.; "NIHES-SNPs, environmental genome project, NIEHS ES15478, Department of Genome Sciences, Seattle, WA [URL: http://egp.gs.washington.edu]." ; Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.	RA	RX: Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Riede M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung M.-W., Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D., Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D., Schatzkowitz W.S., Sherwood J.K., Wittrak L.A., Nickerson D.A.; "NIHES-SNPs, environmental genome project, NIEHS ES15478, Department of Genome Sciences, Seattle, WA [URL: http://egp.gs.washington.edu]." ; Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
RA	RN: SEQUENCE FROM N.A. (ISOFORM ALPHA).	RN	SEQUENCE FROM N.A. (ISOFORM ALPHA).
RA	RX: MEDLINE=12388157; PubMed=12477932; DOI=10.1073/pnas.242603899;	RX	SEQUENCE FROM N.A. (ISOFORM ALPHA).
RA	RA: Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D., Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D., Schatzkowitz W.S., Sherwood J.K., Wittrak L.A., Nickerson D.A.; "NIHES-SNPs, environmental genome project, NIEHS ES15478, Department of Genome Sciences, Seattle, WA [URL: http://egp.gs.washington.edu]." ; Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.	RA	RA: Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D., Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D., Schatzkowitz W.S., Sherwood J.K., Wittrak L.A., Nickerson D.A.; "NIHES-SNPs, environmental genome project, NIEHS ES15478, Department of Genome Sciences, Seattle, WA [URL: http://egp.gs.washington.edu]." ; Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
RA	RA: Sequence B', Hoffmann J., Holtz J., Schulz R., Heusch G., Darmer D., Name=bak; Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.	RA	RA: Sequence B', Hoffmann J., Holtz J., Schulz R., Heusch G., Darmer D., Name=bak; Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RA	DR: EMBL: AJ001204; CAA04398.1; GO: GO:0042981; P:regulation of apoptosis; IEA.	RA	DR: EMBL: AJ001204; CAA04398.1; GO: GO:0042981; P:regulation of apoptosis; IEA.
RA	DR: InterPro: IPR000012; Bcl2 BH.	RA	DR: InterPro: IPR000012; Bcl2 BH.
RA	DR: InterPro: IPR0002475; BCL2family.	RA	DR: InterPro: IPR0002475; BCL2family.
RA	DR: Pfam: PF00452; Bcl-2_1.	RA	DR: Pfam: PF00452; Bcl-2_1.
RA	DR: PROSITE: PS00062; BCL2_FAMILY; 1.	RA	DR: PROSITE: PS00062; BCL2_FAMILY; 1.
RA	DR: NON_TER: PS01259; BH3_1.	RA	DR: NON_TER: PS01259; BH3_1.
RA	FT: 1 FT: 80 SEQUENCE 80 AA: 8818 MN: FD1AF83BD7D9C86 CRC64;	RA	FT: 1 FT: 80 SEQUENCE 80 AA: 8818 MN: FD1AF83BD7D9C86 CRC64;
RA	Query Match 35.4%; Score 390; DB 2; Length 80;	RA	Query Match 35.4%; Score 390; DB 2; Length 80;
RA	Best Local Similarity 92.5%; Pred: No. 4, 4e-27; Indels 0; Gaps 0;	RA	Best Local Similarity 92.5%; Pred: No. 4, 4e-27; Indels 0; Gaps 0;
RA	Matches 74; Conservative 3; Mismatches 3; Indels 0; Gaps 0;	RA	Matches 74; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullally S.J., RA
 Bosak S.A., McIwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., RA
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., RA
 Villaon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., RA
 Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., RA
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., RT
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., RT
 Rodriguez A.C., Grinowicz J., Schmutz J., Myers R.M., RT
 Butterfield Y.S.N., Krzywinski M.I., Smailus D.E., RN
 Schein A., Schein J.E., Jones J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 [7] SEQUENCE OF 1-131 FROM N.A. (ISOFORM ALPHA), AND VARIANTS
 RP SEQUENCE OF 1-131 FROM N.A. (ISOFORM ALPHA), AND VARIANTS
 RP NON-HODGKIN'S LYMPHOMA SEP-59 AND ILE-93.
 MEDLINE=92096610; PubMed=1339999;
 RX Tanaka S., Louie D.C., Kant J.A., Reed J.C., "Frequent incidence of somatic mutations in translocated BCL2
oncogenes of non-Hodgkin's lymphomas.", Blood 79:229-237 (1992).
 [8] RN
 RP SUBCELLULAR LOCATION
 RX MEDLINE=91066924; PubMed=2250705;
 RA Hockenberry D., Nunez G., Milliman C., Schreiber R.D., Kornmeyer S.J.;
 RT "Bcl-2 is an inner mitochondrial membrane protein that blocks
programmed cell death.", Nature 348:334-336 (1990).
 RT
 RN [9]
 RP MTAGENESIS
 RX MEDLINE=94249528; PubMed=8183370;
 RA Yin X.-M., Oltvai Z.N., Kornmeyer S.J.;
 RT "Bcl-1 and BH2 domains of Bcl-2 are required for inhibition of apoptosis
and heterodimerization with Bax.", Nature 369:321-323 (1994).
 [10] RN
 RP CLEAVAGE BY CASPSES, AND MUTAGENESIS.
 RX MEDLINE=91204466; PubMed=94540;
 RA Cheng E.-H.-Y., Kirsch D.G., Clem R.J., Ravi R., Kastan M.B., Bedi A.,
 RA "Bcl-2 is an inner mitochondrial membrane protein that blocks
programmed cell death.", Nature 369:321-323 (1994).
 RT
 RN [11]
 RP INTERACTION WITH TP53BP2.
 RX MEDLINE=96251339; PubMed=8668206;
 RA Naumovski L., Cleary M.L.;
 RT "The p53-binding protein 53BP2 also interacts with Bcl12 and impedes
cell cycle progression at G2/M.", Mol. Cell. Biol. 16:3884-3892 (1996).
 RN [12] RP REVIEW ON PHOSPHORYLATION.
 RX MEDLINE=921260650; PubMed=11368354;
 RA Ryvolova P.P., Deng X., May W.S.;
 RT "Phosphorylation of Bcl12 and regulation of apoptosis.";
 RN Leukemia 15:15-52 (2001).
 RN [13] RP PHOSPHORYLATION BY ASKL/JNK1.
 RX MEDLINE=9036804; PubMed=1967572;
 RA Yamamoto K., Ichijo H., Kornmeyer S.J.;
 RT "Bcl-2 is phosphorylated and inactivated by an ASKL/Jun N-terminal
protein kinase pathway normally activated at G(2)/M.", Mol. Cell. Biol. 19:8419-8418 (1999).
 RL "FUNCTION: Suppresses apoptosis in a variety of cell systems
including factor-dependent lymphohematopoietic and neural cells.
Regulates cell death by controlling the mitochondrial membrane
permeability. Appears to function in a feedback loop system with
caspases. Inhibits caspase activity either by preventing the
release of cytochrome C from the mitochondria and/or by binding to
the apoptosis-activating factor (APAF-1)."
 CC -!- SUBUNIT: Forms homodimers, and heterodimerizes with BAX, BAD, BAK and
 CC BCL-X(L). Heterodimerization with BAX requires intact BH1 and BH2
 CC domains, and is necessary for anti-apoptotic activity (By
 CC similarity). Also interacts with APAF-1, RAF-1 and TP53BP2.

CC -!- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular
membrane of the nuclear envelope and the endoplasmic reticulum.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=Alpha;
 CC Iso1=P10415-1; Sequence=Displayed;
 CC Name=Beta;
 CC Iso1=P10415-2; Sequence=VSP 000512;
 CC -!- TISSUE SPECIFICITY: Expressed in a variety of tissues.
 CC -!- DOMAIN: The BH4 domain is required for anti-apoptotic activity and
for interaction with RAF-1.
 CC -!- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl12
anti-apoptotic activity. Growth factor-stimulated phosphorylation on Ser-70 by PKC is required for the anti-apoptotic activity and
occurs during the G2/M phase of the cell cycle. In the absence of
growth factors, Bcl12 appears to be phosphorylated by other protein
kinases such as ERKs and stress-activated kinases.
 CC Dephosphorylated by protein phosphatase 2A (PP2A) (By similarity).
 CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
cleaved protein, lacking the BH4 domain, has pro-apoptotic
activity, causes the release of cytochrome C into the cytosol
promoting further caspase activity.
 CC -!- DISEASE: Involved in follicular lymphoma (FL) (also known as type
I Chronic lymphatic leukemia) by a chromosomal translocation
t(14;18)(q32;q21) which involves BCL2 and immunoglobulin gene
regions. BCL2 mutations found in non-Hodgkin's lymphomas carrying
the chromosomal translocation could be attributed to the Ig
somatic hypermutation mechanism resulting in nucleotide
transitions.
 CC -!- SIMILARITY: Belongs to the Bcl-2 family.
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
 CC -!- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
 CC WWW="http://www.infobio.gen.fr/services/chromocancer/Genes/BCL2ID49.html".
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
 CC -!- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
 CC WWW="http://www.infobio.gen.fr/services/chromocancer/Genes/BCL2ID49.html".
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
 CC -!- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
 CC WWW="http://www.infobio.gen.fr/services/chromocancer/Genes/BCL2ID49.html".
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
 CC -!- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
 CC WWW="http://www.infobio.gen.fr/services/chromocancer/Genes/BCL2ID49.html".
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
 CC -!- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
 CC WWW="http://www.infobio.gen.fr/services/chromocancer/Genes/BCL2ID49.html".
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
 CC -!- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
 CC WWW="http://www.infobio.gen.fr/services/chromocancer/Genes/BCL2ID49.html".
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
 CC -!- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
 CC WWW="http://www.infobio.gen.fr/services/chromocancer/Genes/BCL2ID49.html".
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
 CC -!- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
 CC WWW="http://www.infobio.gen.fr/services/chromocancer/Genes/BCL2ID49.html".
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
 CC -!- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
 CC WWW="http://www.infobio.gen.fr/services/chromocancer/Genes/BCL2ID49.html".
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
 CC -!- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
 CC WWW="http://www.infobio.gen.fr/services/chromocancer/Genes/BCL2ID49.html".
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
 CC -!- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
 CC WWW="http://www.infobio.gen.fr/services/chromocancer/Genes/BCL2ID49.html".
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
 CC -!- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
 CC WWW="http://www.infobio.gen.fr/services/chromocancer/Genes/BCL2ID49.html".
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
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Db 10 DNREIYKTHYKLSQRGYEWDAQDVGAAAPGAAAPGAFSSQPGHTPHPAASRDPVART 69
 Qy 63 LPLO_PSTINGQVGQLAI-----GDDINRRTDSEBFOTMLHQPTAENAYEY 110
 CC
 Db 70 SPLQTPAPAAAGPALSPPVVLHTRQAGDDESRVRRDFAEMSSOLHLPFTAGR 129
 Qy 111 PTKIATSLFEGGINGRVVALLGFGRYRLAHVYQHGLTFLQVTRFYVDFMLHCIAWR 170
 Db 130 PATVYBELLFRDGIVNGRIVAFFFGVMCVYESNREMSPLVNDTIALWTEYLNRH-LHTW 188
 Qy 171 IAQRGGWVAALNLGNCP1-----LANTLVVIGVVLG 201
 Db 189 IQDNGGWDADFVEL-YGPMRMRPLFDTSWLSLKTLSSLALVG 227

RESULT 13
BCL2_BOVIN STANDARD; PRT; 229 AA.
 ID BCL2_BOVIN STANDARD; PRT; 229 AA.
 AC O02718;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Apoptosis regulator Bcl-2.
 GN Name=BCL2;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 NX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=F Holstein; TISSUE=Thymus;
 RX MEDLINE=98162380; PubMed=9501056;
 RA Reyes R.A., Cockrell G.L.;
 RT "Increased ratio of bcl-2/pax expression is associated with bovine leukemia virus-induced leukemogenesis in cattle.";
 RL Virology 242:184-192 (1998).
 CC -: FUNCTION: Suppresses apoptosis in a variety of cell systems including factor dependent lymphohematopoietic and neural cells.
 CC Regulates cell death by controlling the mitochondrial membrane permeability. Appears to function in a feedback loop system with caspases. Inhibits caspase activity either by preventing the release of cytochrome c from the mitochondria and/or by binding to the apoptosis-activating factor (APAF-1) (By similarity).
 CC -: SUBUNIT: Forms homodimers, and heterodimers with BAX, BAK and Bcl-X(L). Heterodimerization with BAX requires intact BH1 and BH2 domains, and is necessary for anti-apoptotic activity. Also interacts with APAF-1, RAF-1 and TP53BP2 (By similarity).
 CC -: SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular membrane of the nuclear envelope and the endoplasmic reticulum (By similarity).
 CC -: DOMAIN: The BH4 domain is required for anti-apoptotic activity and for interaction with RAF-1 (By similarity).
 CC -: PTM: Phosphorylation/diphosphorylation on Ser-63 regulates Bcl-2 anti-apoptotic activity. Growth factor-stimulated phosphorylation on Ser-63 by PKC is required for the anti-apoptosis activity and occurs during the G2/M phase of the cell cycle (By similarity). In the absence of growth factors, Bcl-2 appears to be phosphorylated by other protein kinases such as ERKs and stress-activated kinases. Dephosphorylated by protein phosphatase 2A (PP2A) (By similarity).
 CC -: PTM: Proteolytically cleaved by caspases during apoptosis. The cleaved protein, lacking the BH4 domain, has pro-apoptotic activity, causes the release of cytochrome c into the cytosol promoting further caspase activity (By similarity).
 CC -: SIMILARITY: Belongs to the Bcl-2 family.
 CC -: SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
 CC -: SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
 CC -: SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
 CC -: SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.

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 CC
 Db 129 U92434; AAB53319; 1; -
 DR IPR006712; Bcl2_BH.
 DR InterPro; IPR003093; Bcl2_BH4.
 DR InterPro; IPR003475; Bcl2_Family.
 DR InterPro; IPR004725; Bcl2_reg.
 DR Pfam; PF00452; Bcl-2_1.
 DR Pfam; PF02180; BH4_1.
 DR TIGRFAMS; TIGR00865; bcl-2_1.
 DR PROSITE; PS50062; Bcl2_FAMILY_1.
 DR PROSITE; PS501080; BH1_1.
 DR PROSITE; PS01258; BH2_1.
 DR PROSITE; PS01259; BH3_1.
 DR PROSITE; PS01260; BH4_1_1.
 DR PROSITE; PS50063; BH4_2_1.
 KW Apoptosis; Mitochondrion; Phosphorylation; Transmembrane.
 FT DOMAIN 10 30 BH4.
 FT DOMAIN 64 68 Poly_Pro.
 FT DOMAIN 69 72 Poly_Ala.
 FT DOMAIN 83 97 BH3.
 FT DOMAIN 126 145 BH1.
 FT DOMAIN 177 192 BH2.
 FT TRANSEM 202 223 Potential.
 FT SITE 34 35 Cleavage (by caspases) (By similarity).
 FT MODE_RS 63 63 PhosphaSerine (By PKC) (By similarity).
 SQ SEQUENCE 229 AA; 25099 MW; ADDDOA98FFFFID CRC64;
 Query Match 16 9%; Score 186; DB 1; Length 229;
 Best Local Similarity 26 2%; Pred. No. 2.6e-08;
 Matches 55; Conservative 30; Mismatches 85; Indexes 40; Gaps 7;
 Qy 30 DTEEVRSYYFYRHQQ-----EQEAEAV-----AAPAD-----PEMYTLPQPS 68
 Db 10 DNREIYKTHYKLSQRGYEWDAQDVGAAAPGAFSSQPGHTPHPAASRDPVART 120
 Qy 69 STMGCQ-----VERQLAIGDDINRRTDSEBFOTMLHQPTAENAYEYFTKIAITS 120
 Db 70 AAAGGAPSPSPVPPVHTLRLQAGDFDSRYRDFAMESSOLHLPPTFABERFATVVEELR 129
 Qy 121 SGINNGRVALLGFGYRVALHYQHGLTFLQVTRFYVDFMLHCTARWIAQRGHWAA 180
 Db 130 DGVNGRIVAFFERGQMVVESVREMSLVDSIALWMTBYLNHR-LHTWIDQNGWDAF 188
 Qy 181 LNLNGNPI-----LNVLYVGGVLLG 201
 Db 189 VEL-YGPMRMRPLFDTSWLSKLALLSLAVG 217

RESULT 14
BCLX_CHICK STANDARD; PRT; 229 AA.
 ID BCLX_CHICK STANDARD; PRT; 229 AA.
 AC Q07816; Q99008;
 DT 01-NOV-1997 (Rel. 31, Created)
 DT 05-JUL-2004 (Rel. 44, Last sequence update)
 DB Apoptosis regulator Bcl-X (Bcl-2-like 1 protein).
 GN Name=BCL2L1; Synonyms=COLX, BCL-X;
 OS Gallus gallus (Chicken).
 OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM SHORT).
 RX MEDLINE=93364977; PubMed=835789;
 RA Boile L.H., Gonzalez-Garcia M., Nunez G., Postema C.E., Thompson C.B.;
 RA Turka L.A., Mao X., Nunez G., Thompson C.B., Ding L., Lindsten T.,

"bcl-x", a bcl-2-related gene that functions as a dominant regulator of apoptotic cell death.";
 Cell 74:597-608(1993).
 [2]
 SEQUENCE FROM N.A. (ISOFORM LONG).
 STRAIN=Hubbard White Mountain; TISSUE=Testis;
 MEDLINE=9764485; PubMed=9110311;
 Villagrassa X., Mezquita C., Mezquita J.;
 RT "Differential expression of bcl-2 and bcl-x during chicken spermatogenesis."
 RT Mol. Reprod. Dev. 47:26-29(1997).
 -!- FUNCTION: Dominant regulator of apoptotic cell death. The long form displays cell death repressor activity, whereas the short isoform promotes apoptosis (By similarity).
 CC SUBCELLULAR LOCATION: Mitochondrial membranes and perinuclear envelope (By similarity).
 -!- ALTERNATIVE PRODUCTS:
 CC Name=Long;
 ID=Q07816-1; Sequence=Displayed;
 CC Name=Short;
 CC ISOID=Q07816-2; Sequence=VSP_000514;
 CC TISSUE SPECIFICITY: Highest expression in organs with lymphoid development. Intact BH1 and BH2 domains are required for anti-apoptotic activity (By similarity).
 -!- SIMILARITY: Belongs to the Bcl-2 family.
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.

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EMBL: Z23110; CAA80657.1; -;
 DR EMBL; AA007677.1; -;
 DR FIR; A47537; A47537.
 HSSP; P53563; 1A73.
 DR InterPro; IPR000712; Bcl12_BH.
 DR InterPro; IPR003093; Bcl12_BH4.
 DR InterPro; IPR002415; BCL2_reg.
 DR PRO0452; Bcl-2; 1.
 DR Pfam; PF02188; BH1; 1.
 DR TIGRFAM; PS500085; bcl-2; 1.
 DR PROSITE; PS50062; BCL2_FAMILY; 1.
 DR PROSITE; PS01080; BH1; 1.
 DR PROSITE; PS01258; BH2; 1.
 DR PROSITE; PS01259; BH3; 1.
 DR PROSITE; PS01260; BH4; 1; 1.
 DR PROSITE; PS50063; BH4; 1; 1.
 KW Alternative splicing; Apoptosis; Transmembrane.
 FT DOMAIN 4 BH4.
 FT DOMAIN 82 96 BH1.
 FT DOMAIN 125 144 BH2.
 FT DOMAIN 176 191 BH2.
 FT TRANSMEM 206 223 Potential.
 FT VARSPLIC 185 229 ERFDLYGNAAMELRKGQETENKWLITGAVGVLIGLSLRSK

LSRK->VRALP (in isoform Short). /FTId=VP_000514;
 SQ SEQUENCE 229 AA; 25733 MW; A97D3X4D04C0E9DA CRC64;
 Query Match 16.7%; Score 184; DB 1; Length 229;
 Best Local Similarity 23.9%; Pred. No. 3.9e-08;
 Matches 55; Conservative 33; Mismatches 92; Indels 50; Gaps 6;

27 VAQDTBEVRSYVFYRHCO-----EQAEQ---VAAPADPENV----- 61
 DB 1 MSSSNRPLVIDEVSYLSSQRGHCSBLEEDENRTDAAEAMDSVLNGSPSHPPPGHIV 60
 62 -----TLPLOQPSSTMGGYGROLAIIGDDINRYDFEFOTMLQHQJQTAENAYEYFT 112
 QY 61 VNGATVHRSSELEVHEVTRASDVROAIRDSEFEIYRRAFSDSLTSQIITPTGTYAQSE 120
 DB 113 KIATSLPESGINWRGYVALLGFGYRLAHYQHGLTGFLGQTVTFVDFMHLHCTARNIA 172
 QY 121 QVYNELPHDGYNWGR-TVAFSGGALVESYDKENRVLGRIVSMTYLDH-LDPWIQ 179
 DB 173 QRGGVW-----AANLNLGNP-----ILNVLVLYGTVLLGFGFVYR 207
 DB 180 ENGGWERFVDLYGNNAAELRKQETENKWLITGAVGVLIGLSLRSK 229
 -!
 Event=Alternative splicing; Named isoforms=2;
 BCL2_CHICK STANDARD; PRT; 233 AA.
 ID BCL2_CHICK; STANDARD; PRT; 233 AA.
 AC Q00709; 000709; 000709;
 DT 01-APR-1993 (Rel. 1. 25, Created)
 DT 01-APR-1993 (Rel. 1. 25, Last sequence update)
 DT 05-JUL-2004 (Rel. 1. 44, Last annotation update)
 DE Apoptosis regulator Bcl-2;
 GN Name=BCL2; Synonyms=BCL-2;
 OS Gallus Gallus (Chicken);
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 RN [1] TAXID=9031;
 RN SEQUENCE FROM N.A.
 RP RX
 RX MEDLINE=92379084; PubMed=1508712;
 RA Eguchi Y., Ewert D.L., Tsujimoto Y.; Isolation and characterization of the chicken bcl-2 gene: expression in a variety of tissues including lymphoid and neuronal organs in adult and embryo.;
 RT Nucleic Acids Res. 20:4187-4192(1992).
 RL [2]
 RN SEQUENCE FROM N.A.
 RP RX
 RX TISSUE=B-cell lymphoma;
 RX MEDLINE=92379084; PubMed=1511008;
 RA Casals-Hatem D.L., Louie D.C., Tanaka S., Reed J.C.; Molecular cloning and DNA sequence analysis of cDNA encoding chicken homologue of the Bcl-2 oncogene.",
 RT Biochim. Biophys. Acta 1132:109-113 (1992).
 -!- FUNCTION: Suppresses apoptosis in a variety of cell systems including factor-dependent lymphohemopoietic and neural membrane. Regulates cell death by controlling the mitochondrial membrane permeability. Appears to function in a feedback loop system with caspases. Inhibits caspase activity either by preventing the release of cytochrome C from the mitochondria and/or by binding to the apoptosis activating factor (APAF-1).
 CC -!- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and BCL-X(L). Heterodimerization with BAX requires intact BH1 and BH2 domains, and is necessary for anti-apoptotic activity (By similarity). Also interacts with APAF-1 and RAF-1 (By similarity).
 CC -!- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular membrane of the nuclear envelope and the endoplasmic reticulum.
 CC -!- TISSUE SPECIFICITY: In adult chicken expressed, in thymus, spleen, kidney, heart, ovary and brain, with the highest levels in all tissues with thymus. In the embryo, highly levels expressed in all tissues with high levels in the bursa of Fabricius.
 CC -!- DOMAIN: The BH4 domain is required for anti-apoptotic activity and for interaction with RAF-1 (By similarity).
 CC -!- SIMILARITY: Belongs to the Bcl-2 family.
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
 CC -!- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
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DR    EMBL; D11382; BAA01978_1;
DR    EMBL; D11381; BAA01178_1; JOINED.
DR    EMBL; Z11961; CA07018_1;
DR    PIR; A37332; A37332.
DR    PIR; S24390; S24390.
DR    HSSP; P10415; 1G5M.
DR    InterPro; IPR000712; Bc12_BH.
DR    InterPro; IPR003093; Bc12_BH4.
DR    InterPro; IPR002475; Bc12_family.
DR    InterPro; IPR004725; Bc12_rgr.
DR    Pfam; PF00452; Bc12_2;
DR    Pfam; PF02180; BH4_1;
DR    TIGRFAMS; TIGR00865; bcl1-2; 1.
DR    PROSITE; PS50062; BCL2_FAMILY; 1.
DR    PROSITE; PS01010; BH1; 1.
DR    PROSITE; PS01258; BH2; 1.
DR    PROSITE; PS01259; BH3; 1.
DR    PROSITE; PS01260; BH4_1; 1.
DR    PROTOCOSIS; PS50063; BH4_2; 1.
KW    Apoptosis; Mitochondrion; Transmembrane.
FT    DOMAIN; 10; BH4.
FT    DOMAIN; 30; BH4.
FT    DOMAIN; 67; BH3.
FT    DOMAIN; 101; BH3.
FT    DOMAIN; 130; 149; BH1.
FT    DOMAIN; 181; 196; BH2.
FT    TRANSMEM; 208; 228; Potential.
FT    CONFLICT; 64; 64; E -> S (in Ref. 2).
FT    CONFLICT; 67; 82; GSAAAEVPPAEGIRP -> ARLLIVRCPRLRGCA (in
Ref. 2).
FT    CONFLICT; 121; 121; H -> T (in Ref. 2).
FT    CONFLICT; 139; 139; G -> V (in Ref. 2).
SQ    SEQUENCE; 233 AA; 25687 MW; 52555ACB6E4C3D CRCG4;
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Query Match Score 183.5; DB 1; Length 233;
 Best Local Similarity 16.6%; Pred. No. 4.4e-08;
 Matches 57; Conservative 35; Mismatches 87; Indels 33; Gaps 10;

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Qy    2 ASGGQG-PGPPRQECPGEALPSASEEQVAQDTEBEVERSYYFVRHQOEAEGVAAAPDPE 59
Db    31 AAGGDRPPVP-----APAP-PAAPAAA-----AGASSHRPPPGSAAASEVPPA 77
Qy    60 MVTPPLQPSSTMGOVGRQLAI--IGDDINRRYDSEFQMLQHLOPTABNAVEYFTKATS 117
Db    78 EGLRPAPP-----GVHLALRQDGDEFSSRYQDFAGMSGQHLHTPTAHRFRVAVVE 130
Qy    118 LFESGINNGRVVALGFGRVLALHVQYQGLTGELGQYPRFVDFMLIHCIAWIAORGGW 177
Db    131 LFRDGVNNGRIVAFFEGGVMCVESVNREMSPLVDNIAWWTEYLNRH-LHNWIQDNGW 189
Qy    178 VAAINL-GNG--PI----LINVIVLGVVLLG 201
Db    190 DAFVELYGNNSMRPLDFDSWISLTILSYLVG 221
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Search completed: December 6, 2004, 16:11:48
 Job time : 196 sec

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GenCore version 5.1.6
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OM protein - protein search, using sw model
 Run on: December 6, 2004, 16:03:06 ; Search time 38 Seconds
 (without alignments)
 534.256 Million cell updates/sec

Title: US-09-633-200-7
 Perfect score: 1103
 Sequence: 1 MASQGPGPRQEGEPAF.....LVLGVVLLGQFVVRFFKS 211
 Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 28416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing First 45 summaries

Database : PIR:79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	1103	100.0	211	2 S58873	Bak protein - human
2	1075	97.5	211	2 S58875	bcl-2 protein - human
3	189.5	17.2	205	1 TVHUB1	transforming protein
4	189	17.1	239	1 TVHUAI	transforming protein
5	183.5	16.6	233	2 A7332	transforming protein
6	181	16.4	233	2 I49056	bcl-x long - mouse
7	180	16.3	233	2 B47537	bcl-X protein - rat
8	178.5	16.2	199	1 TVMSB1	apoptosis regulator
9	178	16.0	236	1 TVMSA1	transforming protein
10	177	16.0	236	2 I53744	gene bcl-2 protein
11	176.5	16.0	236	2 B37332	transforming protein
12	174.5	15.8	216	2 I67431	bcl-X-long - rat
13	173.5	15.7	233	2 JC7383	B-cell lymphoma 2
14	172.5	15.6	236	2 JC7382	bcl-2 - rat (fram
15	170.5	15.5	236	2 A47537	apoptosis regulator
16	167.5	15.2	190	2 A47538	bcl-2-associated p
17	164	14.9	227	2 JE0203	bcl-2-associated p
18	160.5	14.6	232	2 S24390	bcl-X transmembrane
19	158.5	14.4	214	2 I49057	bcl-2-associated p
20	146	13.2	218	2 B47538	bcl2 homolog MCL1
21	143.5	13.0	350	2 A47476	bcl-2-associated p
22	143	13.0	192	2 D47539	bcl-2-associated p
23	143	13.0	192	2 A47538	bax-delta protein
24	142	12.9	179	2 JC7255	bcl-2-associated p
25	126	11.4	133	2 I53295	gene bcl-2 protein
26	122	11.1	154	2 I58194	hemopoietic specific
27	116	10.5	172	2 I39055	Bcl-2 related - hu
28	112	10.2	175	2 I39055	bcl-2-associated p
29	109	9.9	143	2 I38921	

Total number of hits satisfying chosen parameters:

283416

ALIGNMENTS

RESULT 1	S58873	Bak protein - human
		N/A; Alternate names: bcl-2 homolog;cdn-1 protein
	C;Species: Homo sapiens (man)	
	C;Date: 15-Feb-1996 #sequence revision 01-Mar-1996 #text_change 09-Jul-2004	
	C;Accession: S58873; S58872; S58874	
	R;Chittenden, T.; Harrington, E.A.; O'Connor, R.; Flemington, C.; Lutz, R.J.; Evan, G.I.	
	Nature 374: 733-736, 1995	
	A;Title: Induction of apoptosis by the Bcl-2 homologue Bak.	
	A;Reference number: S58873; 6666	
	A;Accession: S58873	
	A;Status: preliminary; nucleic acid sequence not shown	
	A;Molecule type: mRNA	
	A;Residues: 1-211 <CHI>	
	A;Cross-references: UNIPROT:Q16611; ENZY:U23765; NID:975897; PID:AAA93066.1; PMID:9758	
	R;Farrow, S.N.; White, J.H.M.; Martinou, J.; Raven, T.; Pun, K.T.; Grinham, C.J.; Marti	
	Nature 374: 736-739, 1995	
	A;Title: Cloning of a bcl-2 homologue by interaction with adenovirus E1B 19K.	
	A;Reference number: S58872; PMID:715729	
	A;Accession: S58872	
	A;Status: Preliminary	
	A;Molecule type: mRNA	
	A;Residues: 1-211 <PAR>	
	A;Cross-references: EMBL:X84213; NID:9804984; PID:9804985	
	R;Kiefer, M.C.; Brauer, M.J.; Powers, V.C.; Wu, J.J.; Umansky, S.R.; Tomei, L.D.; Barr,	
	Nature 374: 736-739, 1995	
	A;Title: Modulation of apoptosis by the widely distributed Bcl-2 homologue Bak.	
	A;Reference number: S58874; PMID:95231654; PMID:715731	
	A;Accession: S58874	
	A;Status: preliminary	
	A;Molecule type: mRNA	
	A;Residues: 1-11 <KIE>	
	A;Cross-references: EMBL:U16811; NID:9595923; PID:AAA74466.1; PMID:9595924	
	C;Genetics:	
	A;Gene: GB:BAK	
	A;Cross-references: GDB:635887	
	Query Match Score 100.0%; Best Local Similarity 100.0%; Matches 211; Conservat	
	0; Mis matches 0; Indels 0; Gaps 0;	
	Length 211; Pre. No. 8.3e-93;	
Qy	1 MASQQGPQPGPQECPALPSASEQVAQDTBEYFRSYFYRHQEQAEGVAPADPEM 60	
Db	1 MASQQGPQPGPQECPALPSASEQVAQDTBEYFRSYFYRHQEQAEGVAPADPEM 60	
Qy	61 VTLPLQPSSTMGQYRQLAIGDDNRRYDSEFCMLQHQIOPTEAYFTKIAATSLFE 120	
Db	61 VTLPLQPSSTMGQYRQLAIGDDNRRYDSEFCMLQHQIOPTEAYFTKIAATSLFE 120	
Qy	121 SGINNGRVVALLGFYRFLAHVYQHGLTGFQVTRYVDFMGHCIARWIAORGWVAA 180	

Db	121 SGINWGRVVALLGFGYRLAHIVYQHGLTGFLGQVTRFVVDFMLHHCIARWIAQRGGWVA 180	A;Accession: D37332 A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation
Qy	181 LNlNGNPILNVLGVVLGQFVVRFFKS 211	A;Molecule type: DNA A;Residues: 1-33,'E',34-95,'T',97-109,'R',111-205 <EGU>
Db	181 LNlNGNPILNVLGVVLGQFVVRFFKS 211	C;Genetics: A;Gene: GDB:BCL2 A;Cross-references: GDB:119031; OMIM:151430 A;Map Position: 18q21.3-18q21.3
	RESULT 2	C;Function: A;Description: blocks apoptosis in hematopoietic cells C;Superfamily: bcl apoptotic regulator, inhibitor type C;Keywords: alternative splicing; apoptosis; B-cell lymphoma; follicular lymphoma; proto-oncogene
	55875 cdn-2 Protein - human	C;Species: Homo sapiens (man) C;Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004 C;Accession: S58875 C;Reference number: 558875 A;Accession: S58875 A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-211 <KLB> A;Cross-references: UNIPROT:Q13014; EMBL:UL6812; PIDN:AAA74467.1; PMID:95955 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1994
Query Match	Score 1075; DB 2; Length 211+;	Query Match 17.2%; Score 189.5; DB 1; Length 205; Best Local Similarity 27.4%; Pred. No. 8.1e-10; Matches 54; Conservative 27; Mismatches 73; Indels 43; Gaps 7;
Db	1 MASGQQPDPQQCGEADLPSASEEQVQAQDDEEVFSYVSYHQQEQAGAAAPADPM 60	Qy 30 DTBEVFRSYVFYHQO--EQFAEGV-----AAPA-----DPEMVT 62 Db 10 DNREBIVKHYKLSQGYENDAGDVGAAPGAAAPPGIFSSQPGHTPHAAASRDPPVART 69
Qy	1 MASGQQPDPQQCGEADLPSASEEQVQAQDDEEVFSYVSYHQQEQAGAAAPADPM 60	Qy 63 LPLQ-PSSTMGQYGRQLAI-----GDDINRNYDSEFQTMQLQHJQPTAENAYE 110 Db 70 SPQTAAAGPAISPVPPVTHLRLQGDDFRRYRDFDAEMSSQLHLTPFTGR 129
Query Match	97.5%; Score 1075; DB 2; Length 211+;	Query Match 11.1%; Score 189.5; DB 1; Length 205; Best Local Similarity 97.2%; Pred. No. 2.9e-90+; Matches 205; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
Db	1 MASGQQPDPQQCGEADLPSASEEQVQAQDDEEVFSYVSYHQQEQAGAAAPADPM 60	Qy 111 FTKIATLISFESSGGINWGRVVALLGFGYRLAHIVYQHGLTGFLGQVTRFVVDMLHHCIARW 170 Db 130 FAVVEELFRDQGNWGRIVAFFEGGMVCESVNRENSPLVDNIALMTENRHLHTW 188
Qy	1 VTLPLQPSSTMGQYGRQLAIQDDINRNYDSEFQTMQLQHJQPTAENAYEFTKIASLPE 120	RESULT 4 TVHUAL
Db	1 VTLPLQPSSTMGQYGRQLAIQDDINRNYDSEFQTMQLQHJQPTAENAYEFTKIASLPE 120	Transforming protein bcl-2, splice form alpha - human C;Species: Homo sapiens (man) C;Date: 31-Dec-1988 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004 C;Accession: C37332; A29409; S02452; A24428; A27622; B27622 R;Tsujimoto, Y.; Ewert, D.L.; Tsujimoto, Y. Nucleic Acids Res. 20, 4187-4192, 1992 A;Title: Isolation and characterization of the chicken bcl-2 gene: expression in a variety of tissues A;Reference number: A37332; PMID:1508712 A;Accession: C37332 A;Status: nucleic acid sequence not shown; not compared with conceptual translation A;Molecule type: DNA A;Residues: 1-239 <EGU>
Qy	121 SGINWGRVVALLGFGYRLAHIVYQHGLTGFLGQVTRFVVDMLHHCIARWIAQRGGWVA 180	A;Cross-references: UNIPROT:PI0415 A;Note: this report is a correction R;Tsujimoto, Y.; Croce, C.M. Proc. Natl. Acad. Sci. U.S.A. 83, 5214-5218, 1986 A;Title: Analysis of the structure, transcripts, and protein products of bcl-2, the gene for transforming protein bcl-2, splice form beta - human A;Reference number: A29409; PMID:3523487 A;Accession: A29409; MUID:86259760; PMID:3523487 A;Molecule type: mRNA A;Residues: 1-95,'A,'96-'A', '97-109,'G,'111-236,'S,'238-239 <TSU> A;Cross-references: GB:MI3949; NID:GL7936; PMID:AAA51813.1; PMID:9179367 A;Note: this sequence has been corrected in reference A37332 R;Seto, M.; Jaeger, U.; Hockett, R.D.; Graninger, W.; Bennett, S.; Goldman, P.; Korsmeyer, R.Tanaka, S.; Louis, D.C.; Kant, J.A.; Reed, J.C. EMBO J. 7, 123-131, 1988 A;Title: Alternative promoters and exons of somatic mutations and deregulation of the Bcl-2 gene A;Reference number: S02452; PMID:88196071; PMID:2834197 A;Accession: S02452 A;Molecule type: mRNA A;Residues: 1-239 <SET> R;Cleary, W.L.; Smith, S.D.; Sklar, J. Cell 47, 19-38, 1986 A;Cross-references: GB:S72602; NID:9241046; PMID:AAD14111.1; PMID:94261811 A;Title: Cloning and structural analysis of cDNAs for bcl-2 and a hybrid bcl-2/immunogl A;Reference number: A24428; PMID:87002488; MUID:2857599 A;Title: Isolation and characterization of the chicken bcl-2 gene: expression in a variety of tissues A;Reference number: A37332; PMID:92375724; PMID:1508712 A;Residues: 1-58,'T',60-116,'R',118-239 <CLE>
Qy	181 LNlNGNPILNVLGVVLGQFVVRFFKS 211	Db 152566; PMID:92096610; PMID:1339299 A;Accession: 152566 A;Molecule type: DNA A;Residues: 1-131 <TAN> A;Cross-references: GB:S72602; NID:9241046; PMID:AAD14111.1; PMID:94261811 R;Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y. Nucleic Acids Res. 20, 4187-4192, 1992 A;Title: Isolation and characterization of the chicken bcl-2 gene: expression in a variety of tissues A;Reference number: A37332; PMID:92375724; PMID:1508712 A;Residues: 1-58,'T',60-116,'R',118-239 <CLE>

A;Cross-references: GB:W14745; NID:919370; PID:AAA15591.1; PID:9179371
 R;Hu, C.; Zorn, S.; Jensen, J.P.; Coupland, R.W.; Ko, H.S.; Wright, J.J.; Bakhshi, A.
 Oncogene Res. 2, 263-275, 1988
 A;Title: Consequences of the t(14;18) chromosomal translocation in follicular lymphoma:
 A;Reference number: A27622; MUID:88217344; PMID:3285301
 A;Accession: A27622
 A;Molecule type: mRNA
 A;Residues: 1-58; 'T' 60-239 <HUA>
 A;Accession: B27622
 A;Molecule type: DNA
 A;Residues: 1'-6; 'S' 8-58; 'T' 60-128; 'C' 130-239 <HUA2>
 A;Note: the sequence was determined from the germline gene
 C;Comment: Constitutive expression of BCL2 following t(14;18) chromosomal translocation
 C;Genetics:
 A;Gene: GDB:BCL2
 A;Cross-references: GDB:119031; OMIM:151430
 A;Map position: 18q11.3-18q21.3
 C;Function:
 A;Description: blocks apoptosis in hematopoietic cells
 C;Superfamily: bcl apoptosis regulator, inhibitory type
 C;Keywords: alternative splicing; apoptosis; B-cell lymphoma; follicular lymphoma; proto
 Query Match 17.1% Score 189; DB 1; Length 239;
 Best Local Similarity 26.4% Pred. No. 1.1e-09;
 Matches 59; Conservative 31; Mismatches 81; Indels 50; Gaps 8;
 QY 30 DTEEVFRSYFYRHOQ---EAEARGV----AAPA-----DPEMVT 62
 DB 10 DNRELVVMRTHYKUSQRGEWDAADGVAAAPGAAAPGIFSSQDGHTEPAASRDPPART 69
 QY 63 LPLQ-PSSTMGQVGRQLALL-----GDDINRKYDSEFQTMHQIQTARENAYE 110
 DB 70 SPLQTAAAGAAAGAPSVPVVTHLTRQAGDDFSRYYRDRDAEMSSQLHITPFTARGR 129
 QY 111 FTKLATSLFESGINWGRVVALLGFGYRALHYQHGLTGELQVTRFVDFMLHHCTARW 170
 DB 130 FATVVEELFRDGGVTRIAFFERGGVNCVESYNTREMPLVDNIALMTVEYNRH-LHTW 188
 QY 171 IAQRGGWVAALNLNGPI-----LNVLYVGVVILG 201
 DB 189 IQDNQGWDAAFEVEL-YGPSSMRPLFEDWSLKLTLSSLALVG 227

RESULT 6

bcl-x long - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
 C;Accession: I49056; S52866
 R;Pang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.
 J. Immunol., 153, 4388-4393, 1994
 A;Title: Cloning and molecular characterization of mouse bcl-x in B and T lymphocytes.
 A;Reference number: I49055; MUID:95052604; PMID:7963517
 A;Accession: I49056
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-233 <RBS>
 A;Cross-references: UNIPROT:064373; EMBL:U10101; NID:9506647; PID:AAA82173.1; PID:95056
 R;Kameyaki, H.; Michaud, G.Y.; Takatsu, K.; Okura, M.
 submitted to the EMBL Data Library, November 1994
 A;Description: IL-5 inhibits anti-IGM-induced apoptosis in an immature B cell line thro
 A;Reference number: S52866
 A;Accession: S52866
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Cross-references: EMBL:X83574; NID:9695622; PID:CAA58557.1; PID:9695623
 A;Residues: 1-233 <RBS>
 C;Superfamily: bcl apoptosis regulator, inhibitory type
 Query Match 16.4% Score 181; DB 2; Length 233;
 Best Local Similarity 28.3%; Pred. No. 5.7e-09;
 Matches 43; Conservative 23; Mismatches 70; Indels 16; Gaps 3;
 QY 71 MGQVGRQLAIGDDINRKYDSEFQTMHQIQTARENAYEFTKIASLPESGINWGRVVA 130
 DB 83 YAAVROALRAGDDEBLLRRAFSNLTSQHLIPTGTYAQSFQVNELFRDGTINWGRIVA 142
 QY 131 LLGFGRYRALHYQHGLTGELQVTRFVDFMLHHCTARWQGQWYAALNL-GNGP- 187
 DB 143 FFSFGGALCVESVDKEMQVLVRSWATYLNDH-LEPWIQENGWDTFVDLYNNAAA 201
 QY 188 -----LNVLYVGVVILGQFVYRR 207
 DB 202 ESRKGQBERFRNRWFELTGMVAGVVLGSLSFRK 233

RESULT 7

BCL-X protein - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Accession: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
 C;Accession: S51761; S51762
 R;Michaelidis, T.M.;
 submitted to the EMBL Data Library, November 1994
 A;Reference number: S51761
 A;Accession: S51761
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-233 <CMIC>
 A;Cross-references: UNIPROT:F5356; EMBL:X82537; PID:CAA57886.1; PID:9607176
 A;Experimental source: embryonic; brain
 A;Accession: S51762
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-125,189-233 <MI2>

A;Cross-references: UNIPROT:Q00709; EMBL:D11381
 C;Genetics:
 C;Superfamily: bcl apoptosis regulator, inhibitory type
 C;Keywords: mitochondrion; transforming protein; transmembrane protein
 Query Match 16.6% Score 183.5; DB 2; Length 233;
 Best Local Similarity 26.9% Pred. No. 3.4e-09;
 Matches 57; Conservative 35; Mismatches 87; Indels 33; Gaps 10;
 QY 2 ASQQG-#PGPRPQECGEALPSASEEQQAQDDEEVFRSYVFRHQQEAVAAADE 59
 DB 31 AAGDRPYP-----APAPALAPAPAATA-----AGASSHHRPEPGSAAASEVPAA 77
 QY 60 MVTRPLQPSSTMGQVGRQLAI--IGDDINRKYDSEFQTMHQIQTARENAYEFTKIASLPESGINWGRVVA 117

A;Cross-references: EMBL:X82537; NID:9607176; PIDN:CAA57887.1; PID:9607178
 A;Experimental source: embryonic; brain
 A;Note: smaller form due to splicing
 C;Genetics:
 A;Introns: 125/3
 C;Superfamily: bcl apoptosis regulator, inhibitory type
 Query Match Score 16.4%; Best Local Similarity 28.3%; Matches 43; Conservative 23; Mismatches 70; Indels 16; Gaps 3;
 Qy 71 MGQYGRQLIIGDDINRYDSEFQTMQLQHQLQTAENAYEFTKIASTLSEFSGIVNGRVA 130
 Db 83 MAAVKQALREAGDEFEYLRRRAFSDLTSQLHTPTGAYQSEFQVYNELFRDGVNNGRIV 142
 Qy 131 LLFGYRLAHVYQHGLTGFLQVTRFVDFMHHCTARWIAQRGGWVAALNL-SNGP - 187
 Db 143 FFSRGALCQEVSDKEMQVLVSRIASMATLINDH-LEPMHQENGWDTFTDLYNNAAA 201
 Qy 188 -----TINVLVVLGVYLLGQFVVR 207
 Db 202 ESSKGQEEFNRWFLTGHTVAGVVLGSLLSFRK 233

RESULT 8

B47537 apoptosis regulator bcl-xL - human
 N;Alternative names: bcl-2-related protein
 N;Contains: apoptosis regulator bcl-xS
 C;Species: Homo sapiens (man)
 C;Date: 16-Aug-1996 #Sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
 C;Accession: B47537; C47537
 R;Noise: L.H.; Gonzalez-Garcia, M.; Postema, C.E.; Ding, L.; Lindsten, T.; Turka, L.A.;
 A;Title: bcl-x, a bcl-2-related gene that functions as a dominant regulator of apoptotic
 A;Reference number: A47537; MUZD:93364977; PMID:8358789
 A;Accession: B47537
 A;Molecule type: nucleic acid sequence not shown; translated from GB/EMBL/DBJ
 A;Residues: 1-233 <B01>
 A;Cross-references: UNIPROT:Q07817; GB:L20121; NID:9510900; PIDN:CAA80661.1; PID:9510901
 A;Accession: C47537
 A;Status: nucleic acid sequence not shown; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-69, '71-125, 189-233 <B02>
 A;Cross-references: GB:L20122; NID:9623236; PIDN:CRA80662.1; PID:9623237
 C;Genetics:
 A;Gene: GDB:BCL2L
 A;Cross-references: GDB:228079
 C;Superfamily: bcl apoptosis regulator, inhibitory type
 C;Keywords: alternative splicing, apoptosis
 F;1-125,189-233/Product: apoptosis regulator bcl-xL #status predicted <MA2>
 Query Match Score 16.3%; Best Local Similarity 28.3%; Matches 43; Conservative 22; Mismatches 71; Indels 16; Gaps 3;
 Qy 71 MGQYGRQLIIGDDINRYDSEFQTMQLQHQLQTAENAYEFTKIASTLSEFSGIVNGRVA 130
 Db 83 MAAVKQALREAGDEFEYLRRRAFSDLTSQLHTPTGAYQSEFQVYNELFRDGVNNGRIV 142
 Qy 131 LLFGYRLAHVYQHGLTGFLQVTRFVDFMHHCTARWIAQRGGWVAALNL-SNGP - 187
 Db 143 FFSRGALCQEVSDKEMQVLVSRIASMATLINDH-LEPMHQENGWDTFTDLYNNAAA 201
 Qy 188 -----TINVLVVLGVYLLGQFVVR 207
 Db 202 ESRKGQERRPNRFDTGHTVAGVVLGSLLSFRK 233

RESULT 9

TVM81 transforming protein bcl-2-beta - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 31-Dec-1988 #Sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
 C;Accession: B25360
 R;Negrini, M.; Silini, E.; Kozak, C.; Tsujimoto, Y.; Croce, C.M.
 Cell 49, 455-463, 1987
 A;Title: Molecular analysis of mbcl-2: structure and expression of the murine gene homolog
 A;Reference number: A90893; PMID:3032455
 A;Molecule type: DNA
 A;Genetics:
 A;Cross-references: UNIPROT:P10417; GB:M16506; PIDN:AAA37281.1; PID:9387110
 Query Match Score 16.2%; Best Local Similarity 25.1%; Matches 49; Conservative 25; Mismatches 84; Indels 37; Gaps 5;
 Qy 22 ASEEQVAQDTEEVRSYYFYRHQOE---QEAEQVAAAP--ADPEMVTLPLQP-SSTMGQV 74
 Db 2 AQAGRRTGYDNREIVMKYTHYKLSQRGTYENDAGDADAPLGAAPTPGIFSFQPEESNPMPAV 61
 Qy 75 GRQLAI-----TGDINRRYDSEFQTMQLQHLOPATAE 105
 Db 62 HREMAARTSPLRPLVATAGPALSPVPCVHLTLLRACDFSRYYRFAENSSLQHITPPF 121
 Qy 1105 NAYEFKTIATSLSFEGINWGRVVALLGFYRFLAHVYQHGLTGFLQVTRFVVDMLHH 165
 Db 122 TARGREATVVEELFRDGTNWGRIVAFEPFGCTMCVESVNREMSPVLDNTIALWMTEYLNRH 181
 Qy 166 CIARWIAQRGGWVA 180
 Db 182 -LHTWIDQDNGGWVA 195

RESULT 10

TVM81 transforming protein bcl-2-alpha - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 31-Dec-1988 #Sequence_revision 31-Dec-1988 #text_change 28-Jul-2003
 C;Accession: A25960; E37332
 R;Negrini, M.; Silini, E.; Kozak, C.; Tsujimoto, Y.; Croce, C.M.
 Cell 49, 455-463, 1987
 A;Title: Molecular analysis of mbcl-2: structure and expression of the murine gene homolog
 A;Reference number: A90893; PMID:87187643; PMID:3032455
 A;Molecule type: DNA
 A;Genetics:
 A;Cross-references: GB:L31132; GB:M16506; PIDN:AAA37282.1; PID:9387109
 Nucleic Acids Res. 20, 4187-4192, 1992
 R;Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
 A;Title: Isolation and characterization of the chicken bcl-2 gene: expression in a variety of tissues
 A;Accession: B37332
 A;Status: preliminary: nucleic acid sequence not shown; not compared with conceptual translation
 A;Molecule type: DNA
 A;Genetics:
 A;Introns: 1-33, '8,-34-220, 'A1,-223-236 <EGU>
 C;Keywords: alternative splicing, mitochondrion; transforming protein; transmembrane protein

Query Match Score 16.0%; Best Local Similarity 25.1%; Matches 32; Conservative 27; Mismatches 90; Indels 38; Gaps 6;

Qy 22 ASEEQVAQDTEEVRSYYFYRHQOE---QEAEQVAAAP--ADPEMVTLPLQP-SSTMGQV 74
 Db 2 AQAGRRTGYDNREIVMKYTHYKLSQRGTYENDAGDADAPLGAAPTPGIFSFQPEESNPMPAV 61

QY 75 GRQLAI-----IGDINRYDSEFOTMLQHLOPPTAB 105
 Db 62 HREMAARTSPRLPVATAGPALSPPCVCVHTLRRAGDDTSRVRDFAEAMSQHLLPFP 121
 QY 106 NAYEYFTKIASTLFESEGNNGRVALLGFGRYLALHYQHGLTGFQVTRFVDFMLH 165
 Db 122 TARGFRATVVEELFRGGVNRIVAFEEFGGVMCVESVNREMSPLVDNTALWMTTEYLNRH 181
 QY 166 CIARWIAQRGEWAALNLNGNPILAVL 192
 Db 182 -LHTWICDNGERDAFVEL-YEPSKREPL 206

RESULT 11
 153744 gene bcl-2 protein - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 29-May-1998 # sequence_revision 29-May-1998 #text_change 09-Jul-2004
 C;Accession: 153744
 R;Sato, T.; Irie, S.; Krajewski, S.; Reed, J.C.
 Gene 140, 291-292, 1994
 A;Title: Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein.
 A;Reference number: 153744; PMID:9193015; PMID:144041
 A;Accession: 153744
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-36 <RES>
 A;Cross-references: UNIPROT:P49950; GB:L14680; NID:9408946; PIDN:AAA53662.1; PMID:9408947
 C;Genetics:
 A;Gene: bcl-2
 C;Superfamily: bcl apoptosis regulator, inhibitory type

Query Match Score 176.5; DB 2; Length 236;
 Best Local Similarity 24.2%; Pred. No. 1.5e-08;
 Matches 55; Conservative 31; Mismatches 90; Indels 51; Gaps 7;

QY 22 ASBEEQVAQDTEEVFSYVFTRHQQ -----EQEAEQVAAPA----- 56
 Db 2 AQAGRTGYDNREIYMKYTHYKLSQLRGYEWDTGDEDASPLRAAPPGITSFQPESNRTPAV 61
 QY 57 --DPENMVTLPLQPSSTMQGVGRQLAI-----GDDINRYDSEFOTMLQHICPT 103
 Db 62 HRDTAARTSLRP-LVAAAGPALSPPVPHVLTIRRAADDTSRVRDFAEAMSQHLLT 119
 QY 104 AENAYEYFTKIASTLFESEGNNGRVALLGFGRYLALHYQHGLTGFQVTRFVDFML 163
 Db 120 PFTARGFRATVVEELFRGGVNRIVAFEEFGGVMCVESVNREMSPLVDNTALWMTTEYLN 179
 QY 164 HHCIARWIAQRGEWAALNLNGNPILAVL 201
 Db 180 RH-LHTWICDNGERDAFVEL-YGPSMRPLFDFSWLSLCTLLSLALVG 224

Matches 50; Conservative 27; Mismatches 81; Indels 25; Gaps 7;
 QY 2 ASGQG--PGPPROECGBPALPSSEEVQVACDTEEVRSYVYRHQQOEAEGVAAAPADPE 59
 Db 31 AASEDRPRVPP----APA-PAAPAAVA-----AAGASSHHRREPSSAAAEVPPA 77
 QY 60 MYTLPQFSSTMQGVGRQLAI--IGDDINRYDSEFOTMLQHLOPPTAENADEVFTKIAST 117
 Db 78 EGIRPAPP----GTHLARQAGDEFSRKYQDRAQMQLHLPFTAHGRFTAVVE 130
 QY 118 LFESSGINWGRVVALLGFCYRLALHYQHGLTGFQVTRFVDFMLHCTIARWIQRGWN 177
 Db 131 LFRDGWNGRIVAFAFFGGVMCVESVNRENSPLVDNLATWTEYLNRH-LHNWIDQNGGW 189

RESULT 13
 167431 BCL-X-Long - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
 C;Accession: 167431
 RTilly, J.L.; Tilliy, K.I.; Keaston, M.L.; Johnson, A.L.
 Endocrinology 136, 232-241, 1995
 A;Title: Expression of members of the bcl-2 gene family in the immature rat ovary: constitutive bcl-2 and bcl-x long messenger ribonucleic acid levels.
 A;Reference number: 153295; PMID:9512948; PMID:9828536
 A;Accession: I67431
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-233 <RES>
 A;Cross-references: UNIPROT:P53563; EMBL:U34963; NID:91004376; PIDN:AAA77686.1; PMID:91004376
 C;Superfamily: bcl apoptosis regulator, inhibitory type

Query Match Score 173.5; DB 2; Length 233;
 Best Local Similarity 27.6%; Pred. No. 2.7e-08;
 Matches 48; Conservative 25; Mismatches 78; Indels 23; Gaps 5;

QY 49 AEGVAAAPADPEMVTPLQPSSTMQGVGRQLAIIGDDINRYDSEFOTMLQHLOPPTAENY 108
 Db 68 ATGHSSLDAREV-LP-----MAXVKOALREAGDEFLYRRAFSDSLTSQHLHTPGTVY 120
 QY 109 EYFTKATSLPESQGNWGRVVALLGFCYRLALHYQHGLTGFQVTRFVDFMLHCTA 168
 Db 121 QSFEQVYNELFRDGWNGRIVASSSFGGGALCVSYDKENQMLVSRIASNMATYLNHD-JE 179

QY 169 RWIAQRGQGWWAALNT-GNGP-----ILNVLVLVGLGVVLLGGQFVVRR 207
 Db 180 PWIQENGWDTFVDLYGNNTAPESSKGQERFNRFLTGMTVAGVTLGSLFSRK 233

RESULT 14
 JC7383 B-cell lymphoma 2 protein - Chinese hamster
 C;Species: Cricetus griseus (Chinese hamster)
 C;Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 09-Jul-2004
 C;Accession: JC7383
 RTomicic, M.T.; Christmann, M.; Kaina, B.
 Biochem. Biophys. Res. Commun. 275, 889-903, 2000
 A;Title: Cloning and functional analysis of cDNA encoding the hamster Bcl-2 protein.
 A;Reference number: JC7383
 A;Contents: Ovary
 A;Accession: JC7383
 A;Molecule type: mRNA
 A;Residues: 1-236 <TOM>
 A;Cross-references: UNIPROT:Q9JYV8; GB:AJ271720
 C;Comment: This protein has anti-apoptotic function, and supports cell survival.
 C;Genetics:
 A;Gene: bcl-2
 C;Superfamily: bcl apoptosis regulator, inhibitory type

RESULT 12
 B37332 Transforming protein (bcl-2-beta) - chicken
 C;Species: Gallus gallus (chicken)
 C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 28-Jul-2003
 C;Accession: B37332; S55452
 R;Buchi, Y.; Ewer, D.L.; Tsujimoto, Y.
 Nucleic Acids Res. 20, 4187-4192, 1992
 A;Title: Isolation and characterization of the chicken bcl-2 gene: expression in a variety of tissues
 A;Reference number: A37332; PMID:92375724; PMID:1508712
 A;Status: nucleic acid sequence not shown
 A;Molecule type: DNA
 A;Residues: 1-216 <EGI>
 A;Cross-references: EMBL:D11381; EMBL:D11382
 C;Superfamily: bcl apoptosis regulator, inhibitory type

Query Match Score 174.5; DB 2; Length 216;
 Best Local Similarity 27.3%; Pred. No. 2e-08;

C;Keywords: B-cell lymphoma; ovary

Query Match 15.6%; Score 172.5; DB 2; Length 236;
 Best Local Similarity 24.4%; Pred. No. 3.4e-08;
 Matches 55; Conservative 30; Mismatches 93; Indels 47; Gaps 7;
 Qy 22 ASEBQVAQDTEEVFRSYVYRHQQEQ-
 Db 2 AQAGRGTGDNREIWKYKLSQRGYEWVDGVDAAPIGAAPTPGIFSSNPTPAV 61
 Qy 57 -DPEMVTPLQPSSTMGQ------VGRALATIGDDINRYOSEFQMLQHQIQLPTE 105
 Db 62 HRDMAARTSPLRIVATGPTLSPVPPVWHLTIRRAGDDERRYRDFAMNSSQLHLTPF 121
 Qy 106 NAYEYFTKATSLFESGINGRVVALGFGRYRLAHVYQHGLTGFLGQVTRFYVDFMLH 165
 Db 122 TARGFATVVEEFDQGNWGRIVAFFEGGNCVTSVRNRMSPYDNUALWWTEYLHN 181
 Qy 166 CIARWIAQRGGWAAALNIGNGPI-----LNLVVLGVVLLG 201
 Db 182 -LHTWIDQNGWDNAFVEL-YGPSPVRPLDFSMUSLKTLISLAIVG 224

RESULT 15

I67432
 BCL2 - rat (fragment)
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
 C;Accession: I67432
 R;Billy, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L.
 Endocrinology 136, 232-241, 1995
 A;Title: Expression of members of the bcl-2 gene family in the immature rat ovary: equinonistative bcl-1 and bcl-x long messenger ribonucleic acid levels.
 A;Reference: 154295; MUID:95129487; PMID:7828536
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-236 <RES>
 A;Cross-references: UNIPROT:P49950; EMBL:U34964; NID:91004378; PID:AAA77687.1; PID:9100
 C;SuperFamily: bcl apoptosis regulator, inhibitory type

Query Match 15.5%; Score 170.5; DB 2; Length 236;
 Best Local Similarity 23.3%; Pred. No. 5.2e-08;
 Matches 53; Conservative 30; Mismatches 93; Indels 51; Gaps 7;
 Qy 22 ASEBQVAQDTEEVFRSYVYRHQQEQ-
 Db 2 AQAGRGTGDNREIWKYKLSQRGYEWVDGVDAAPIGAAPTPGIFSSNPTPAV 61

Qy 57 -DPEMVTPLQPSSTMGQVGRQLAII-----GDDINRYSEFQMLQHQIQLPTE 103
 Db 62 HRDMAARTSPLRIVATGPTLSPVPPVWHLTIRRAGDDERRYRDFAMNSSQLHLTPF 119
 Qy 104 AENAEYFKIATSLFESGINGRVVALGFGRYRLAHVYQHGLTGFLGQVTRFYVDFML 163
 Db 120 PFTARGFATVVEEFDQGNWGRIVAFFEGGNCVTSVRNRMSPYDNUALWWTEYLHN 179
 Qy 164 HHCTIARWIAQRGGWAAALNIGNGPI-----VNLGVVLLG 201
 Db 180 RH-LHTWIDQNGWDNAFVEL-YGPSPVRPLDFSMUSLKTLISLAIVG 224

Search completed: December 6, 2004, 16:12:32
 Job time : 40 secs

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CM protein - protein search, using sw model

Run on: December 6, 2004, 16:11:57 ; Search time 141 Seconds

(without alignments)
533.570 Million cell updates/sec

Title: US-09-633-200-7

Perfect score: 1103

Sequence: 1 MASGQEGGPPRQECEGPALP.....LWVLGVLIGQQFVRRFFKS 211

Scoring table: BLOSUM62

Gappen 10.0 , Gapext 0.5

Searched: 1582122 seqs, 356623098 residues

Total number of hits satisfying chosen parameters:

1582122

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA: *

1: /cgns2_6_ptodata/1/pubpaas/US07_PUBCOMB.pep:*

2: /cgns2_6_ptodata/1/pubpaas/PCN_NEW_PUB.pep:*

3: /cgns2_6_ptodata/1/pubpaas/US06_NEW_PUB.pep:*

4: /cgns2_6_ptodata/1/pubpaas/PUBCOMB.pep:*

5: /cgns2_6_ptodata/1/pubpaas/US07_NEW_PUB.pep:*

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20: /cgns2_6_ptodata/1/pubpaas/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1103	100.0	211	14	US-10-101-482-7
2	1103	100.0	211	14	US-10-101-482-10
3	1103	100.0	211	14	US-10-109-294-2
4	1103	100.0	211	14	US-10-177-293-25
5	1103	100.0	211	15	US-10-003-632C-6
6	1103	100.0	211	17	US-10-B5-282-34
7	108B.5	98.7	210	14	US-10-101-482-22
8	1075	97.5	211	14	US-10-101-482-9
9	1075	97.5	211	14	US-10-101-482-11
10	625	56.7	117	14	US-10-109-294-4
11	609	55.2	116	14	US-10-109-294-5
12	216	21.4	45	9	US-10-97-980-39
13	214.5	19.4	99	15	US-10-294-445-26

ZIP: 94304-1018
CURRENT APPLICATION DATA:
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
OPERATING SYSTEM: IBM PC Compatible
SOFTWARE: PatentIn Release #1.0, Version #1.3.0

RESULTS
US-10-101-482-7
; Sequence 7, Application US10101482
; Publication No. US2003000837A1
; GENERAL INFORMATION:
; APPLICANT: KIEFER, MICHAEL J.
; ADDRESS: MORRISON & FORSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US-10/101-482
FILING DATE: 18-Mar-2002
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US-08/320,157
FILING DATE: 07-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: LEHARDT, SUSAN K.
REGISTRATION NUMBER: 33-943
REFERENCE/DOCKET NUMBER: 23647-20007.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792

Best Local Similarity 100.0%; Pred. No. 8.6e-101; Mismatches 0; Indels 0; Gaps 0;

Matches 211; Conservative 0; Sequence 1

Qy 1 MASGQQCPGPRQECBAPLPSSEQVADTEEVRSYFVRYQQEQDAEGTAAPADEM 60

Db 1 MASGQQCPGPRQECBAPLPSSEQVADTEEVRSYFVRYQQEQDAEGTAAPADEM 60

Qy 61 VTLPLQPSSTINGQVRQLATIGDIDNRYDSEFQTMLOHQIOPTAENAYEFTKIAATSLE 120

Db 61 VTLPLQPSSTINGQVRQLATIGDIDNRYDSEFQTMLOHQIOPTAENAYEFTKIAATSLE 120

Qy 121 SGINNGRVAALLFGYRLAHVYQHGLTGFGLQVTRVVDFMLHICIAWRIAORGWVA 180

Db 121 SGINNGRVAALLFGYRLAHVYQHGLTGFGLQVTRVVDFMLHICIAWRIAORGWVA 180

Qy 121 SGINNGRVAALLFGYRLAHVYQHGLTGFGLQVTRVVDFMLHICIAWRIAORGWVA 180

Db 121 SGINNGRVAALLFGYRLAHVYQHGLTGFGLQVTRVVDFMLHICIAWRIAORGWVA 180

Qy 181 LNLNQGPILNVLVVGVLLQFVYRRFFKS 211

Db 181 LNLNQGPILNVLVVGVLLQFVYRRFFKS 211

RESULT 4

US-10-177-293-25

Sequence 25, Application US/10177293

Publication No. US20030124128A1

GENERAL INFORMATION:

APPLICANT: Lillie, James

APPLICANT: Glatt, Karen

APPLICANT: Zhao, Xumei

APPLICANT: Gannavarpu, Manjula

APPLICANT: Karatkar, Shubhangi

APPLICANT: Mertens, Maureen

APPLICANT: Myer, Vic

APPLICANT: Wang, Youzhen

APPLICANT: Xu, Yongrac

APPLICANT: Hoersch, Sebastian

APPLICANT: Monahan, John

APPLICANT: Meyers, Rachel E.

APPLICANT: Bast Jr., Robert C.

APPLICANT: Horroabaygi, Gabriel N.

APPLICANT: Pusztai, Lajos

APPLICANT: Meric, Funda

APPLICANT: Sahin, Aysegul

APPLICANT: Mills, Gordon B.

TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT, TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER

FILE REFERENCE: MRI-038

CURRENT APPLICATION NUMBER: US/10/177,293

CURRENT FILING DATE: 2002-06-11

PRIOR FILING DATE: 2001-06-21

PRIOR APPLICATION NUMBER: US 60/301,572

PRIOR FILING DATE: 2001-06-27

PRIOR APPLICATION NUMBER: US 60/306,501

PRIOR FILING DATE: 2001-07-18

PRIOR APPLICATION NUMBER: US 60/325,002

PRIOR FILING DATE: 2002-03-05

PRIOR APPLICATION NUMBER: US 60/362,585

PRIOR FILING DATE: 2002-03-05

PRIOR FILING DATE: 2002-05-14

NUMBER OF SEQ ID NOS: 506

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO: 25

LENGTH: 211

TYPE: PRT

ORGANISM: Homo sapiens

US-10-177-293-25

Query Match 100.0%; Score 1103; DB 104; Length 211;

Best Local Similarity 100.0%; Pred. No. 8.6e-101

Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MASGQQCPGPRQECBAPLPSSEQVADTEEVRSYFVYRRFFKS 211.

PRIOR APPLICATION NUMBER: 08/3178,507
 PRIORITY FILING DATE: 1995-01-26
 PRIOR APPLICATION NUMBER: 08/250,478
 PRIORITY FILING DATE: 1994-05-27
 NUMBER OF SEQ ID NOS: 50
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 34
 LENGTH: 211
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-825-282-34

Query Match 98.7%; Score 1088.5; DB 14; Length 210;
 Best Local Similarity 99.5%; Pred. No. 2.3e-99;
 Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Query Match 98.7%; Score 1088.5; DB 14; Length 210;
 Best Local Similarity 99.5%; Pred. No. 2.3e-99;
 Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Query Match 98.7%; Score 1088.5; DB 14; Length 210;
 Best Local Similarity 99.5%; Pred. No. 2.3e-99;
 Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 MASGQQGPQPROCGEPALPSASEEQAQDTEBEVFRSYVFYRHOEQEARGVAAAPADPEM 60
 Db 1 MASGQQGPQPROCGEPALPSASEEQAQDTEBEVFRSYVFYRHOEQEARGVAAAPADPEM 60
 Qy 1 MASGQQGPQPROCGEPALPSASEEQAQDTEBEVFRSYVFYRHOEQEARGVAAAPADPEM 60
 Db 1 MASGQQGPQPROCGEPALPSASEEQAQDTEBEVFRSYVFYRHOEQEARGVAAAPADPEM 60
 Qy 61 VTLPLQPSSTMQVGROLAIGDDINRYDSEFQTMQLQHLOPTAENAYEYFTKIAATSLE 120
 Db 61 VTLPLQPSSTMQVGROLAIGDDINRYDSEFQTMQLQHLOPTAENAYEYFTKIAATSLE 120
 Qy 61 VTLPLQPSSTMQVGROLAIGDDINRYDSEFQTMQLQHLOPTAENAYEYFTKIAATSLE 120
 Db 61 VTLPLQPSSTMQVGROLAIGDDINRYDSEFQTMQLQHLOPTAENAYEYFTKIAATSLE 120
 Qy 121 SGINWGRVVALLGFGYMLAHYQHGILTGFQVTRVVDFMLHHCIARNIAORGCVWA 180
 Db 121 SGINWGRVVALLGFGYMLAHYQHGILTGFQVTRVVDFMLHHCIARNIAORGCVWA 180
 Qy 121 SGINWGRVVALLGFGYMLAHYQHGILTGFQVTRVVDFMLHHCIARNIAORGCVWA 180
 Db 121 SGINWGRVVALLGFGYMLAHYQHGILTGFQVTRVVDFMLHHCIARNIAORGCVWA 180

RESULT 8
 US-10-101-482-9
 Sequence 9, Application US/10101482
 Publication No. US2003000883A1

GENERAL INFORMATION:
 APPLICANT: KIEFER, MICHAEL C.
 BARR, PHILIP J.

TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA
 ENCODING THE PROTEINS AND METHODS OF USE THEREOF

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORRISON & FOERSTER
 STREET: 755 Page Mill Road
 CITY: Palo Alto
 STATE: California
 COUNTRY: USA
 ZIP: 94304-1018

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 ATTORNEY/AGENT INFORMATION:
 NAME: LEHNHARDT, SUSAN K.
 REGISTRATION NUMBER: 33,943
 REFERENCE/DOCKET NUMBER: 23647-20007.20

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 813-5600
 TELEFAX: (415) 494-0792
 TELEX: 706141

INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 211 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-10-101-482-9

Query Match 97.5%; Score 1075; DB 14; Length 211;
 Best Local Similarity 97.2%; Pred. No. 5.1e-98;
 Matches 205; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MASGQQGPQPROCEGPALPSAEEQVAQDTEEVRSYFVHQQEQEAGAAAPADEM 60
 Db 1 MASGQQGPQPROCEGPALPSAEEQVAQDTEEVRSYFVHQQEQEAGAAAPADEM 60
 Qy 61 VTLPLQPSSTMGQYGRQLATIGDDINRYDSEFQMLQHQOPTAENAYEFTKIAITSLFE 120
 Db 61 VTLPLQPSSTMGQYGRQLATIGDDINRYDSEFQMLQHQOPTAENAYEFTKIAITSLFE 120
 Qy 121 SGINWGRVVALFGYRFLAHIVQGLTGFGLQVTRFYVDFMLHCIARWIAORGWVA 180
 Db 121 SGINWGRVVALFGYRFLAHIVQGLTGFGLQVTRFYVDFMLHCIARWIAORGWVA 180
 Qy 121 SGINWGRVVALFGYRFLAHIVQGLTGFGLQVTRFYVDFMLHCIARWIAORGWVA 180
 Db 121 SGINWGRVVALFGYRFLAHIVQGLTGFGLQVTRFYVDFMLHCIARWIAORGWVA 180

RESULT 9
 US-10-101-482-11
 Sequence 11, Application US/10101482
 Publication No. US2003000883A1
 GENERAL INFORMATION:
 APPLICANT: KIEFER, MICHAEL C.
 BARR, PHILIP J.

TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA NUMBER OF SEQUENCES: 22
 ENCODING THE PROTEINS AND METHODS OF USE THEREOF CORRESPONDENCE ADDRESS:
 ADDRESSSEE: MORRISON & FOERSTER STREET: 755 Page Mill Road CITY: Palo Alto STATE: California COUNTRY: USA ZIP: 94304-1018

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS CURRENT APPLICATION DATA:
 SOFTWARE: PatentIn Release #1.0, Version #1.3.0 APPLICATION NUMBER: US/10/189,294 FILING DATE: 01-Jul-2002 CLASSIFICATION: <Unknown> PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US/10/101,482 APPLICATION NUMBER: US/09/381,488 FILING DATE: 18-Mar-2002 FILING DATE: 11-Feb-2000 ATTORNEY/AGENT INFORMATION:
 CLASSIFICATION: <Unknown> NAME: BROWN, THERESA A. REGISTRATION NUMBER: 32,547 REFERENCE/DOCKET NUMBER: 4147-15-PUS TELECOMMUNICATION INFORMATION:
 NAME: LEINHARDT, SUSAN K. TELEPHONE: (303) 863-9700 TELEFAX: (303) 863-0223 INFORMATION FOR SEQ ID NO: "Bak (delta)2 (delta)TM"
 REGISTRATION NUMBER: 33,943 REFERENCE/DOCKET NUMBER: 23547-20007.20 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 813-5600 TELEFAX: (415) 494-0792 TELEX: 706141 INFORMATION FOR SEQ ID NO: 11:
 LENGTH: 211 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 11:

US-10-101-482-11

Query Match 97.5%; Score 1075; DB 14; Length 211;
 Best Local Similarity 97.2%; Pred. No. 5.1e-98;
 Matches 205; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MASGQQGPQPROCEGPALPSAEEQVAQDTEEVRSYFVHQQEQEAGAAAPADEM 60

Db 1 MGQVGRQLATIGDDINRYDSEFQMLQHQOPTAENAYEFTKIAITSLFE 130
 1 MGQVGRQLATIGDDINRYDSEFQMLQHQOPTAENAYEFTKIAITSLFE 60

Query Match 56.7%; Score 625; DB 14; Length 117;
 Best Local Similarity 100.0%; Pred. No. 8.4e-54;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 71 MGQVGRQLATIGDDINRYDSEFQMLQHQOPTAENAYEFTKIAITSLFE 130
 Db 1 MGQVGRQLATIGDDINRYDSEFQMLQHQOPTAENAYEFTKIAITSLFE 60

Qy 131 LLGGYRLAHVYQHGTLGQTVRVDMLHHCTARNIAQRGWVAALNNGP 187
 Db 61 LLGGYRLAHVYQHGTLGQTVRVDMLHHCTARNIAQRGWVAALNNGP 117

RESULT 11

; GENERAL INFORMATION:
 ; APPLICANT: Weiner, David B.
 ; APPLICANT: Yang, Joo-Sung
 ; TITLE OF INVENTION: Compositions and Methods of Using Capsid Protein From Flaviviruse
 ; TITLE OF INVENTION: Pestiviruses
 ; FILE REFERENCE: UPD-4105
 ; CURRENT APPLICATION NUMBER: US/09/971,980
 ; CURRENT FILING DATE: 2001-10-04
 ; PRIOR APPLICATION NUMBER: 60/237,885
 ; PRIOR FILING DATE: 2000-10-04
 ; NUMBER OF SEQ ID NOS: 73
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 39
 ; LENGTH: 45
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: No. US20020164349A1; Sequence US-09-971-980-39

Query Match 21.4%; Score 236; DB 9; Length 45;
 Best Local Similarity 100.0%; Pred. No. 7.7e-16; Indels 0; Gaps 0;

Qy 163 LHHCIAARTAQRGWVAALNLNGPILVVLGVVLLGQFVRR 207
 Db 1 LHHCIAARTAQRGWVAALNLNGPILVVLGVVLLGQFVRR 45

RESULT 13

; GENERAL INFORMATION:
 ; APPLICANT: Godrik, Adam
 ; APPLICANT: Reed, John C.
 ; TITLE OF INVENTION: POLYPEPTIDES, ENCODING NUCLEIC ACID MOLECULES, AND RELATED
 ; TITLE OF INVENTION: BACTERIAL BCL-2 DOMAIN-CONTAINING
 ; TITLE OF INVENTION: POLYPEPTIDES, ENCODING NUCLEIC ACID MOLECULES, AND RELATED
 ; TITLE OF INVENTION: METHODS
 ; FILE REFERENCE: P-LJ 5489
 ; CURRENT APPLICATION NUMBER: US/10/294,445
 ; CURRENT FILING DATE: 2002-11-13
 ; PRIOR APPLICATION NUMBER: US 60/332,964
 ; PRIOR FILING DATE: 2001-11-13
 ; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: FastSeq For Windows Version 4.0
 ; SEQ ID NO: 26
 ; LENGTH: 99
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: synthetic construct

US-10-294-445-26

Query Match 19.4%; Score 214.5; DB 15; Length 99;
 Best Local Similarity 41.7%; Pred. No. 3e-13; Indels 1; Gaps 1;
 Matches 40; Conservative 19; Mismatches 36; Other 1;

Qy 82 GDDINRYDSEFQTMQLHQPTAENAYBFYTKIATSLUFESGINWGRVYALLFGYRALH 141
 Db 5 GDEELKRYVERFSMAVQHLITPELTARLFTQAGEEFSDQGNWGRVYALLFGGAAKK 64

RESULT 14

; GENERAL INFORMATION:
 ; APPLICANT: Morris, David W.
 ; Sequence 1936, Application US/10087192
 ; Publication No. US20020182586A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Morris, David W.

US-10-087-1936

Query Match 14.2%; Score 177; DB 177
 Best Local Similarity 100.0%; Pred. No. 3.2e-52; Indels 0; Gaps 0;

Qy 96 MLQHQPTAENAYBFYTKIATSLUFESGINWGRVYALLFGYRALHVGHTGFGLGVT 155
 Db 1 MLQHQPTAENAYBFYTKIATSLUFESGINWGRVYALLFGYRALHVGHTGFGLGVT 60

Query Match 14.2%; Score 177; DB 177
 Best Local Similarity 100.0%; Pred. No. 3.2e-52; Indels 0; Gaps 0;

Qy 156 RPYVDEMFLHHCTARNIAQRGWVAALNLNGPILVVLGVVLLGQFVRRFFKS 211
 Db 61 RPYVDEMFLHHCTARNIAQRGWVAALNLNGPILVVLGVVLLGQFVRRFFKS 116

RESULT 14

; Sequence 1936, Application US/10087192
 ; Publication No. US20020182586A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Morris, David W.

US-10-087-1936

Query Match 14.2%; Score 1980-39; DB 1980-39
 Best Local Similarity 100.0%; Pred. No. 3.2e-52; Indels 0; Gaps 0;

Qy 156 LVNSAMEGLYVSRLADWWYEFKLHN-LAEWIQONGW 99
 Db 65 LVNSAMEGLYVSRLADWWYEFKLHN-LAEWIQONGW 99

i APPLICANT: Engelhardt, Eric K.
 i TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
 i CANCER
 i FILE REFERENCE: 5245300122
 i CURRENT APPLICATION NUMBER: US/10/087,192
 i PRIORITY FILING DATE: 2002-03-01
 i PRIOR APPLICATION NUMBER: US 09/747,377
 i PRIOR APPLICATION NUMBER: US 09/798,586
 i PRIOR FILING DATE: 2001-03-02
 i NUMBER OF SEQ ID NOS: 2059
 i SOFTWARE: FastSEQ for Windows Version 4.0
 i SEQ ID NO: 1956
 i LENGTH: 205
 i TYPE: PRT
 i ORGANISM: Homo sapiens
 i US-10-087-192-1956

Query Match 17.4%; Score 192; DB 13; Length 205;
 Best Local Similarity 27.7%; Pred. No. 1..4e-10;
 Matches 53; Conservative 25; Mismatches 73; Indels 40; Gaps 6;
 Qy 30 DTEEVPRSYFYRHOO---EQAEGV----AAPA-----DPEMVT 62
 Db 10 DNREIIVMKYIHYKLSQRGYEWDAIDGVGAAPGAAAPGCFSSQGHTHPAASRDPTVRT 69
 Qy 63 LPLQ-PSTMQVGVRQIAII----GDDINRYDSEFQTMLOHLQOPTAENAYEY 110
 Db 70 SPLQTAPAAAGPALSPPVPHLTLRQAGDDESRRDFAEMSSQLHPTPTAGR 129
 Qy 111 FTKIATSLFSFGINGRVAALLGFYRALKHVYQHGLTFLGCVTREFVDFMLHHCTARW 170
 Db 130 PATVVEELFRDGIVNGRIVAFFEGGMCVESNREMSPLVNDNALWMEYLNRH-LHTW 188
 Qy 171 IAORGWVAAL 181
 Db 189 IQDNQGWVGAL 199

RESULT 15
 US-10-148-953A-4
 i Sequence 4, Application US/10148953A
 i Publication No. US 2004/0053428A1
 i GENERAL INFORMATION:
 i APPLICANT: SHIBAZAKI, FUTOSHI
 i TITLE OF INVENTION: APOPTOSIS-INHIBITING POLYPEPTIDES, GENES AND POLYNUCLEOTIDES
 i FILE REFERENCE: 7388/73088
 i CURRENT APPLICATION NUMBER: US/10/148,953A
 i PRIOR APPLICATION NUMBER: PCT/JP00/08657
 i PRIOR FILING DATE: 2000-12-07
 i PRIOR APPLICATION NUMBER: JP 11/350427
 i PRIOR FILING DATE: 1999-12-09
 i NUMBER OF SEQ ID NOS: 21
 i SOFTWARE: PatentIn Ver. 2.1
 i SEQ ID NO: 4
 i LENGTH: 219
 i TYPE: PRT
 i ORGANISM: Artificial Sequence
 i FEATURE:
 i OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 i OTHER INFORMATION: Modified Bcl-2 protein
 i US-10-148-953A-4

Query Match 17.4%; Score 192; DB 15; Length 239;
 Best Local Similarity 26.4%; Pred. No. 1..7e-10;
 Matches 58; Conservative 31; Mismatches 81; Indels 50; Gaps 8;
 Qy 30 DTEEVPRSYFYRHOO---EQAEGV----AAPA-----DPEMVT 62
 Db 10 DNREIIVMKYIHYKLSQRGYEWDAIDGVGAAPGAAPISSOPGHTPHAAASRDPTVRT 69

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 6, 2004, 15:54:19 ; Search time 152 Seconds
(without alignments)
497.973 Million cell updates/sec

Title: US-09-633-200-7

Perfect score: 1103

Sequence: 1 MASQQPGPPROEGEPALE.....LVIIGVLLGQFVTRFFKS 211

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:
1: geneseqP1980s;*
2: geneseqP1990s;*
3: geneseqP2000s;*
4: geneseqP2001s;*
5: geneseqP2002s;*
6: geneseqP2003aa;*
7: geneseqP2003bb;*
8: geneseqP2004s;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	100.0	211	2	AAR77876	Aar77876 Human Cdn
2	1103	100.0	211	AAR81451	Aar81451 Bcl-1 apo
3	1103	100.0	211	AAW03668	AAW03668 Bak proto
4	1103	100.0	211	AAW79534	AAW79534 Bak polyp
5	1103	100.0	211	AAY05433	AAY05433 Human BAK
6	1103	100.0	211	ABB892374	ABB892374 Human BAK
7	1103	100.0	211	AAE37655	AAE37655 Bcl-2 rela
8	1103	100.0	211	ABR47397	ABR47397 Breast ca
9	1103	100.0	211	ADD93300	ADD93300 Human pro
10	1103	100.0	211	ADL60830	ADL60830 Human Bak
11	1103	100.0	211	ADL65726	ADL65726 Human Bcl
12	1075	97.5	211	AAR77877	Aar77877 Human Cdn
13	1075	97.5	211	AAW03669	AAW03669 Bak-2 pro
14	946	85.8	211	ADP04114	ADP04114 Human col
15	829.5	75.2	208	AAY05432	AAY05432 Mouse BAK
16	791	71.7	152	AAR77879	Aar77879 Human Cdn
17	737	66.8	141	AAR77880	Aar77880 Human Cdn
18	625	56.7	117	AAW79535	AAW79535 Truncated
19	609	55.2	116	AAR77881	Aar77881 Human Cdn
20	609	55.2	116	AAW79536	AAW79536 Truncated
21	368	33.4	77	AAB35127	Adh18941 Human ce-
22	284	25.7	52	AAB35127	Ab335127 Mammalian
23	284	25.7	52	AAU76550	Aau76550 Murine Ba
24	214.5	19.4	99	ADL17046	ADL17046 Bcl-2 dom
25	192	17.4	239	AAG64038	Aag64038 Human Bcl

ALIGNMENTS					
RESULT 1					
ID	AAR77876	standard; protein; 211 AA.			
XX					
AC	AAR77876;				
XX					
DD	25-MAR-2003	(revised)			
DD	21-NOV-1995	(first entry)			
XX					
DE	Human Cdn-1.				
XX					
KW	Cdn-1; apoptosis modulator; adoptive immunotherapy; hepatocyte; HIV; autoimmune disease; reperfusion injury; hepatitis; shock;				
KW	lymphoma; eczema.				
XX					
OS	Homo sapiens.				
XX					
PN	WO9515084-A1.				
XX					
PD	08-JUN-1995.				
XX					
PF	30-NOV-1994;	94WO-US013930.			
XX					
PR	30-NOV-1993;	93US-00150067.			
XX					
PR	07-OCT-1994;	94US-0030157.			
XX					
PA	(LXR-B-) LXR BIOTECHNOLOGY INC.				
XX					
PI	Kieffer MC, Barr PJ;				
XX					
DR	WPI: 1995-215106/28.				
DR	N-PSDB; ARQ592.				
XX					
CC	Cdn-1 cDNA was isolated from a human heart cDNA library using a previously isolated clone as probe. Recombinant Cdn-1 was produced in Sf9 and human colon adenocarcinoma HEK29 cells. Expression of Cdn-1 in WI-L2 lymphoblastoid cells resulted in increased cell survival in response to anti-Fas-mediated apoptosis. (Updated on 25-MAR-2003 to correct PN Field.)				
CC					
CC	Sequence 211 AA;				
CC					

Query Match 100.0%; Score 1103; DB 2; Length 211;
 Best Local Similarity 100.0%; Pred. No. 1.4e-112;
 Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MASGQGCPGPROCGEPA LPSASEEQVAQDTEEVFRSYVYFTRHQEQAEQGVAA PADPEM 60
 Db 1 MASGQGCPGPRQECGEPA LPSASEEQVAQDTEEVFRSYVYFTRHQEQAEQGVAA PADPEM 60

Qy 61 VTLPLQSSSTMQVGROLAIIQDDINRYYSEFQTMQHQHOPTA NAYEFTKIA TSLFE 120
 Db 61 VTLPLQSSSTMQVGROLAIIQDDINRYYSEFQTMQHQHOPTA NAYEFTKIA TSLFE 120

Qy 121 SGINWGRVVALGFGRILAHVYQHGTGFLGQVTRFVDFMLHHCIA RMAQRGWVA A 180
 Db 121 SGINWGRVVALGFGRILAHVYQHGTGFLGQVTRFVDFMLHHCIA RMAQRGWVA A 180

Qy 181 LN LGNGPILNVLVLGVLGOFVRRFFKS 211
 Db 181 LN LGNGPILNVLVLGVLGOFVRRFFKS 211

Qy 181 LN LGNGPILNVLVLGVLGOFVRRFFKS 211
 Db 181 LN LGNGPILNVLVLGVLGOFVRRFFKS 211

RESULT 2
 AAR81451 standard; protein; 211 AA.
 ID AAR81451
 XX
 AC AAR81451;
 XX
 DT 02-JUL-1996 (first entry)
 XX
 DE Bcl-X apoptosis-related protein.
 XX
 KW Bcl-X; apoptosis; cell proliferation; cell death; diagnosis; therapy.
 XX
 Homo sapiens.
 XX
 Key
 FT Domain 188..205-
 /label= C-terminal_domain
 /note= "putative membrane localisation sequence"
 XX
 Location/Qualifiers
 FT
 PN WO9605232-A1.
 XX
 PD 22-FEB-1996.
 XX
 PF 09-AUG-1995;
 XX
 PR 09-AUG-1994;
 PR 11-OCT-1994;
 XX
 PA (IMMU-) IMMUNOGEN INC.
 XX
 PI Chittenden TD;
 XX
 DR WPI:1996-139648/14.
 DR N-PSDB; AATI17375.
 XX
 PT New isolated human Bcl-X protein - used to develop prods. for treating
 disorders characterised by inappropriate cell proliferation or cell
 death.
 XX
 PS Claim 3; Fig 4; 10Opp; English.

CC Bcl-X protein (AAR81451) is a member of the Bcl-2 family and can induce
 apoptosis in cells and function as a negative regulator of Bcl-2
 function. Bcl-X mRNA was detected in all human tumour cell lines examined
 and is also widely expressed in primary human tissues. It can be obt. by
 expression of a full-length cDNA clone (AATI1735) in pref. mammalian host
 cells. Bcl-X can be used to develop prods. for treating disorders
 associated with inappropriate cell proliferation or cell death, and to
 raise antibodies used for the diagnosis or monitoring of such disorders

CC Sequence 211 AA;

XX
 Query Match 100.0%; Score 1103; DB 2; Length 211;
 Best Local Similarity 100.0%; Pred. No. 1.4e-112;
 Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MASGQGCPGPROCGEPA LPSASEEQVAQDTEEVFRSYVYFTRHQEQAEQGVAA PADPEM 60
 Db 1 MASGQGCPGPRQECGEPA LPSASEEQVAQDTEEVFRSYVYFTRHQEQAEQGVAA PADPEM 60

Qy 61 VTLPLQSSSTMQVGROLAIIQDDINRYYSEFQTMQHQHOPTA NAYEFTKIA TSLFE 120
 Db 61 VTLPLQSSSTMQVGROLAIIQDDINRYYSEFQTMQHQHOPTA NAYEFTKIA TSLFE 120

Qy 121 SGINWGRVVALGFGRILAHVYQHGTGFLGQVTRFVDFMLHHCIA RMAQRGWVA A 180
 Db 121 SGINWGRVVALGFGRILAHVYQHGTGFLGQVTRFVDFMLHHCIA RMAQRGWVA A 180

Qy 181 LN LGNGPILNVLVLGVLGOFVRRFFKS 211
 Db 181 LN LGNGPILNVLVLGVLGOFVRRFFKS 211

RESULT 3
 AAN03668 standard; protein; 211 AA.
 ID AAN03668
 XX
 AC AAN03668;
 XX
 DT 22-FEB-1997 (first entry)
 DE Bak protein.
 XX
 KW Human; Bak; apoptosis; latency; virus replication; Epstein-Barr virus;
 KW BHRF1; fusion protein; epitope tag; drug screening; co-precipitation;
 KW ELISA; immunoassay; antibody; protein interactive trapping; viricide;
 KW antitumour; diagnostic.
 XX
 Homo sapiens.
 OS WO9633416-A1.
 XX
 PN 24-OCT-1996.
 PD 19-APR-1996;
 XX
 PP 96WO-US005639.
 PR 20-APR-1995;
 XX
 PA (LXR-) LXR BIOTECHNOLOGY INC.
 XX
 PI Barr PJ; Kiefer MC;
 XX
 DR WPI:1996-485886/48.
 DR N-PSDB; AATI2138.
 XX
 PS Screening for anti-viral agents - by detecting the ability of an agent to
 disrupt the interaction of a Bak protein and a viral protein.
 XX
 Disclosure: Fig 1; 24pp; English.
 XX
 This Bak protein sequence represents a bcl-1 homologue which interacts
 with Epstein-Barr virus (EBV) early lytic cycle BHRF1 protein and is
 capable of modulating apoptosis. The protein may be used in complete or
 partial form, or as an epitope tag fusion protein, in a new viricide drug
 screening method, which involves combination of Bak protein and a viral
 protein (e.g. EBV BHRF1), exposure to a test compound, disruption of
 the interaction, e.g. by co-precipitation, protein
 CC interactive trapping or ELISA. Interaction of Bak and viral proteins
 CC allows viral replication or latency in the absence of apoptosis.
 CC Compounds which inhibit the interaction may be used as viricide,
 CC antitumour or diagnostic agents
 XX
 Sequence 211 AA;

Query Match 100.0%; Score 1103; DB 2; Length 211;

Best Local Similarity 100.0%; Pred. No. 1.4e-112;						
Matches	211;	Conservative	0;	Mismatches	0;	Indels
					Gaps	0;
DY	1	MASQGQPQECGPALPASEEQAQDTEEVFSTSYFHRHQEQAEGVAAAPADEM	60			
Db	1	MASQGQPQECGPALPASEEQAQDTEEVFSTSYFHRHQEQAEGVAAAPADEM	60			
DY	61	VTLPLQPSSTMGQVGRQLATIGDDINRYDSEFQMLQHLOPQAENAYEFKTIATSLFE	120			
Db	61	VTLPLQPSSTMGQVGRQLATIGDDINRYDSEFQMLQHLOPQAENAYEFKTIATSLFE	120			
DY	121	SGINNGRVRVALLGFGRYLALHVYQGLTFLGQVTRVUDMLHHCLARWIAQRGWVA	180			
Db	121	SGINNGRVRVALLGFGRYLALHVYQGLTFLGQVTRVUDMLHHCLARWIAQRGWVA	180			
DY	181	LNLNGNPILNVLYLGVVLQFVRRFFKS	211			
Db	181	LNLNGNPILNVLYLGVVLQFVRRFFKS	211			

mono sapiens.

Location/Qualifiers
103 .126
/label= BBPBD-1
/note= "Claim 36"

138 .156
/label= BBPBD-2
/note= "Claim 62"

999841626-A1.

4 SEP-1998.

98WO-US004079.

✓ 3 - MAR-1998;

✓ 13 - MAR-1997;

✓ 9 - JAN-1998;

✓ 98US-0041328P.

✓ 98US-0071097P.

(XRB-) LXR BIOTECHNOLOGY INC.

Liefer MC, Fitzpatrick PA, Gibson HL, Barr PJ;
PSDB; AAV61498.

This is the amino acid sequence of human Bak, a member of the Bcl-2 family that is expressed in heart and other tissues, and which is capable of either killing cells or actively protecting cells from apoptosis, depending on how it interacts with other cellular proteins. A nucleotide sequence (see EAV61498) encoding Bak is provided. The invention relates to a novel Bak binding protein (BRP; see AAW79337). The gene encoding BBR
Disclosure: FIG 2A-C; 77pp; English.

(see AA761499), methods for detecting substances that alter the specific binding between Bak and BBP, as well as diagnostic and therapeutic methods utilising BBP. The invention also encompasses novel Bak-derived peptides, designated BBP binding domains (BBPBDS), and novel nucleotides designated *bbpbpd-1* and *bbpbpd-2* encoding the peptides, which are involved in the interaction between Bak and BBP, and which have been characterised as important death domains of Bak. Modulation of the interaction between proteins that control apoptosis is a major focal point in the treatment of heart disease, viral infection and cancer.

cancer cell a virus infected cell or an autoantibody producing cell. The BH3 polypeptide can be used in therapeutic compositions for treating disease including cancer, other lymphoproliferative conditions, arthritis, inflammation, and autoimmune diseases, which may result from the down regulation of cell death regulation.

Sequence 211 AA;

Query Match 100.0%; Score 1103; DB 2; Length 211;

Best Local Similarity 100.0%; Pred. No. 1.4e-112; Indels 0; Gaps 0;

Matches 211; Conservative 0; Mismatches 0; Gaps 0;

SQ Sequence 211 AA;

```

Qy 1 MASGQQGPSPRQECPGEPALPSASEEQVQAQDTEBEVERSYVFYRHQQFQEARGVAAPADPEM 60
Db 1 MASGQQGPSPSPRQECPGEPALPSASEEQVQAQDTEBEVERSYVFYRHQQFQEARGVAAPADPEM 60
Qy 61 VTLPLQPSSTMGVGRQLAIGDDINRYDSFQTMLOQHLOPTAENAYEFTKATSLSPE 120
Db 61 VTLPLQPSSTMGVGRQLAIGDDINRYDSFQTMLOQHLOPTAENAYEFTKATSLSPE 120
Qy 121 SGINWGRVVALLGFGRYLALHYQHGLTFLGQVTRFVNDMLHICIAARNIAQRGGMWAA 180
Db 121 SGINWGRVVALLGFGRYLALHYQHGLTFLGQVTRFVNDMLHICIAARNIAQRGGMWAA 180
Qy 181 LNQNGPPIVNLVLGIVLLGQFVVRFFKS 211
Db 181 LNQNGPPIVNLVLGIVLLGQFVVRFFKS 211

```

RESULT 6

ABB82374 standard; protein; 211 AA.

XX AC ABB82374;

XX DT 08-JAN-2003 (first entry)

XX DE Human BAK protein sequence.

XX KW BAK; M11L; cytosatic; neuroprotective; nootropic; cerebroprotective.

XX KW apoptosis; human.

XX OS Homo sapiens.

XX PN WO200274908-A2.

XX PD 26-SEP-2002.

XX PP 04-MAR-2002; 2002WO-US006757.

XX PR 02-MAR-2001; 2001US-0273091P.

XX PA (MDSP-) MDS PROTEOMICS INC.

XX PI McFadden G, Moran MF;

XX DR 2002-740855/80.

XX PS Identifying agents which may be potentially pro-apoptotic or anti-apoptotic for treating acute and chronic neurodegenerative diseases, comprising determining the effect of the test agent on complexes of BAK and/or M11L proteins.

XX Disclosure; Fig 11; 83pp; English.

CC The invention relates to identifying agents which may be potentially pro-apoptotic or anti-apoptotic which involves determining the effect of a test agent on the complexes of BAK and/or M11L proteins. The methods are useful for identifying agents which may be potentially pro-apoptotic or anti-apoptotic and for identifying M11L-interacting polyepitopes, and in conducting a target or drug discovery system. The methods are useful for identifying agents capable of inhibiting M11L activity or which can mimic the activity of M11L by inhibiting the activity of BAK and which are

therefore anti-apoptotic agents. Agents identified by the method as involved in regulation of apoptosis may be used in the development of therapeutic agents and methods, and drug screening assays, and in increasing the sensitivity of cancer cells to Chemotherapeutic treatment. Therapeutic applications of apoptosis manipulation include treatment of acute and chronic neurodegenerative diseases, e.g. stroke, Alzheimer's or Huntington's disease by drugs, and sensitization of cancer cells for drug /radiation-induced apoptosis by modulation of survival signals and viral transfer of apoptosis promoting genes. The present sequence represents a human BAK protein.

	Query Match	Score	Length	DB	Best Local Similarity	Pred. No.	Mismatches	Indels	Gaps
Qy	1 MASGQQGPSPRQECPGEPALPSASEEQVQAQDTEBEVERSYVFYRHQQFQEARGVAAPADPEM	100.0%	211	5	100.0%	1.4e-112	0	0	0
Db	1 MASGQQGPSPSPRQECPGEPALPSASEEQVQAQDTEBEVERSYVFYRHQQFQEARGVAAPADPEM	100.0%	211	12	100.0%	1.4e-112	0	0	0
Qy	61 VTLPLQPSSTMGVGRQLAIGDDINRYDSFQTMLOQHLOPTAENAYEFTKATSLSPE	1	120	60	100.0%	1.4e-112	0	0	0
Db	61 VTLPLQPSSTMGVGRQLAIGDDINRYDSFQTMLOQHLOPTAENAYEFTKATSLSPE	1	120	60	100.0%	1.4e-112	0	0	0
Qy	121 SGINWGRVVALLGFGRYLALHYQHGLTFLGQVTRFVNDMLHICIAARNIAQRGGMWAA	61	180	60	100.0%	1.4e-112	0	0	0
Db	121 SGINWGRVVALLGFGRYLALHYQHGLTFLGQVTRFVNDMLHICIAARNIAQRGGMWAA	61	180	60	100.0%	1.4e-112	0	0	0
Qy	181 LNQNGPPIVNLVLGIVLLGQFVVRFFKS	121	211	61	100.0%	1.4e-112	0	0	0
Db	181 LNQNGPPIVNLVLGIVLLGQFVVRFFKS	121	211	61	100.0%	1.4e-112	0	0	0

RESULT 7

	Query Match	Score	Length	DB	Best Local Similarity	Pred. No.	Mismatches	Indels	Gaps
Qy	181 LNQNGPPIVNLVLGIVLLGQFVVRFFKS	121	211	61	100.0%	1.4e-112	0	0	0
Db	181 LNQNGPPIVNLVLGIVLLGQFVVRFFKS	121	211	61	100.0%	1.4e-112	0	0	0

RESULT 7
AAB37655

	Query Match	Score	Length	DB	Best Local Similarity	Pred. No.	Mismatches	Indels	Gaps
Qy	181 LNQNGPPIVNLVLGIVLLGQFVVRFFKS	121	211	61	100.0%	1.4e-112	0	0	0
Db	181 LNQNGPPIVNLVLGIVLLGQFVVRFFKS	121	211	61	100.0%	1.4e-112	0	0	0

XX AC AAB37655;

XX DT 27-AUG-2003 (first entry)

XX DE Bc12 related protein #6.

XX KW Bc12 related protein; growth; protein expression.

XX OS Unidentified.

XX PD WO2003040374-A1.

XX PR 15-MAY-2003..

XX PF 02-NOV-2001; 2001WO-US045553.

XX PR 02-NOV-2001; 2001WO-US045553.

XX PA (CENZ) CENTOCOR INC.

XX PI Lee C, Ly C, Moore G, Shi X;

XX XX WPI; 2003-441576/41.

XX PT New protein expression enhancing Bc12 related nucleic acid for producing commercially useful amounts of expressed protein, comprises a nucleic acid that encodes an expressible protein or at least one Bc12 related protein.

XX Disclosure; Page 52-53; 64pp; English.

XX PT The invention relates to methods and compositions for enhanced protein expression and/or growth of cultured cells using co-transcription of at least one Bc12 related protein encoding nucleic acid molecules. The invention is useful in providing enhanced growth of and/or protein

XX Disclosure; Page 52-53; 64pp; English.

XX PT The invention relates to identifying agents which may be potentially pro-apoptotic or anti-apoptotic which involves determining the effect of a test agent on the complexes of BAK and/or M11L proteins. The methods are useful for identifying agents which may be potentially pro-apoptotic or anti-apoptotic and for identifying M11L-interacting polyepitopes, and in conducting a target or drug discovery system. The methods are useful for identifying agents capable of inhibiting M11L activity or which can mimic the activity of M11L by inhibiting the activity of BAK and which are

CC production from cultured mammalian host cells used for the production of
 CC commercially useful amounts of expressed protein. The present sequence is
 CC Bcl2 related protein
 XX

CC expression of the marker in a control non-breast cancer sample, where a
CC significant increase in the level of expression of the marker in the
CC patient sample and the normal level is an indication that the patient is
CC afflicted with breast cancer. The breast cancer associated sequences from
CC the present invention have cytostatic activities and can be used in gene
CC therapy. The method is useful for diagnosing and treating breast cancer.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published/pct sequences

		XX	Sequence 211 AA;
	SQ	Score 1103; DB 6; Length 211;	
Qy	1	MASGQQGPQPRQECGPALPSAEEQVQAQDTEEVFRSYVFHQQEAEQYAAAPADPEM 60	
Db	1	MASGQQGPQPRQECGPALPSAEEQVQAQDTEEVFRSYVFHQQEAEQYAAAPADPEM 60	
Qy	61	VTLPLQPSSTMQVGROLAIGDDINRYDSEFQTMHQHQLOQTAENAYEYFTKIASTLFE 120	
Db	61	VTLPLQPSSTMQVGROLAIGDDINRYDSEFQTMHQHQLOQTAENAYEYFTKIASTLFE 120	
Qy	121	SGINNGRVALLGFGYRVALHYQHGLTGFLGOVTRVDFMLHHCTARWIAQRGGWVA 180	
Db	121	SGINNGRVALLGFGYRVALHYQHGLTGFLGOVTRVDFMLHHCTARWIAQRGGWVA 180	
Qy	161	LNLNGNPIILNVLYVLGVVLLQGTVRLGFQVVRRFPKS 211	
Db	161	LNLNGNPIILNVLYVLGVVLLQGTVRLGFQVVRRFPKS 211	
RESULT 8			
AER47397	ID	AER47397 standard; protein; 211 AA.	
XX			

AC ABR47397; XX
 DT 12-JUN-2003 (first entry)
 DE Breast cancer associated protein sequence SEQ ID NO:25.
 OS Human; breast cancer; cytosstatic; gene therapy.
 OS Homo sapiens.
 PN WO2003004989-A2.
 PD 16-JAN-2003.
 XX PR 21-JUN-2002; 2002WO-US019669.
 XX PR 21-JUN-2001; 2001US-0299887P.
 PR 27-JUN-2001; 2001US-0301572P.
 PR 18-JUL-2001; 2001US-0306501P.
 PR 25-SEP-2001; 2001US-0325002P.
 PR 05-MAR-2002; 2002US-0362595P.
 PR 14-MAY-2002; 2002US-0380391P.
 XX (MILL-) MILLENIUM PHARM INC.
 XX PI Lillie J, Gammavarapu M, Glatt K, Hoersh S, Kamatkar S, Meyers RE;
 PI Mertens M, Monahan JE, Myer V, Wang Y, Xu Y, Zhao X,
 PI Bast RC, Hortobagyi GN, Pusztai L, Meric F, Sahin A, Mills GB;
 XX DR WPI; 2003-210381/20.
 DR N-PSDB; AC550088.
 XX Breast cancer diagnosis or treatment by comparing the level of expression
 PT of a marker in a patient sample with that in the control non-breast
 PT cancer. PT Determining potential effect of chemotherapeutic agents, useful for
 PT treating cancer, from their ability to induce conformational change in
 Bak protein.

PT Disclosure; SEQ ID NO 1; 16pp; English.
XX The present sequence is the protein sequence of the human pro-apoptotic
CC protein, Bak. A conformational change in the Bak protein is used in the
CC method of the invention for determining the potential effectiveness of a
CC chemotherapeutic compound for treating cancerous cells in a human or
CC animal patient. The method involves: (i) exposing a sample of the
CC compound to the patient to a homohexameric compound
CC taken from the patient's cancerous cells; (ii) assessing whether a patient
CC afflicted with breast cancer, The method comprises comparing the level
CCC of expression of a marker gene, polypeptide, see ACC050334 and
CCC ABR7386 to ABR7632, in a patient sample and the normal
CCC level of the marker gene, polypeptide, see ACC050334 and
CCC ABR7386 to ABR7632, in a control sample.

combination of compounds; and (ii) assaying for a conformational change in the Bak protein of the cells. The conformational change is preferably determined at the N-terminus of Bak or in its BH domain, particularly using a specific binding partner, such as an antibody, for the conformationally altered protein. Conformational change in Bak is a very early (and general) indicator of commitment to apoptosis, occurring before caspase activation, nuclear condensation or cellular blebbing, and is caused by agents that induce apoptosis by different mechanisms. Detecting commitment to apoptosis is a more accurate indicator of activity than cell death and the present method is quicker and simpler than known clonogenic assays.

Sequence 211 AA;

Query Match	Score	DB	Length	AA
Best Local Similarity	100.0%	7	211	
Matches 211; Conservative	100.0%	Pred. No. 1.4e-112		
Mismatches 0; Indels 0; Gaps 0;				
Qy 1 MASCQGPGRPROCGEPALPSASEBQVQAQDTBEVERSYVFYRHQQEAEQVAAPADPEM 60		Db 1 VTLPLQPSSSTMQGVGRQIAIGDINRYDSFQTMQLQHLOPATAENAYEFTKIASTLFE 120		
Db 1 MASCQGPGRPROCGEPALPSASEBQVQAQDTBEVFRSYVFYRHQQEAEQVAAPADPEM 60		Qy 61 VTLPLQPSSSTMQGVGRQIAIGDINRYDSFQTMQLQHLOPATAENAYEFTKIASTLFE 120		
Qy 61 VTLPLQPSSSTMQGVGRQIAIGDINRYDSFQTMQLQHLOPATAENAYEFTKIASTLFE 120		Db 61 VTLPLQPSSSTMQGVGRQIAIGDINRYDSFQTMQLQHLOPATAENAYEFTKIASTLFE 120		
Db 61 VTLPLQPSSSTMQGVGRQIAIGDINRYDSFQTMQLQHLOPATAENAYEFTKIASTLFE 120		Qy 121 SGINWGRVVALLGFGYRLAHYQHGQTGFLGQVTRPVUDFMLHHCTARWAQRGWVA 180		
Qy 121 SGINWGRVVALLGFGYRLAHYQHGQTGFLGQVTRPVUDFMLHHCTARWAQRGWVA 180		Db 121 SGINWGRVVALLGFGYRLAHYQHGQTGFLGQVTRPVUDFMLHHCTARWAQRGWVA 180		
Db 121 SGINWGRVVALLGFGYRLAHYQHGQTGFLGQVTRPVUDFMLHHCTARWAQRGWVA 180		Qy 181 LNLTNGNPILNVLVLLGVVLLGQEVVRFFKS 211		
Qy 181 LNLTNGNPILNVLVLLGVVLLGQEVVRFFKS 211		Db 181 LNLTNGNPILNVLVLLGVVLLGQEVVRFFKS 211		
Db 181 LNLTNGNPILNVLVLLGVVLLGQEVVRFFKS 211				

RESULT 10

ADP60830 standard; protein; 211 AA.

XX

AC ADP60830;

XX DT 12-FEB-2004 (first entry)

XX DE Human Bak #SEQ ID 1.

XX KW Chemotherapeutic; anti-apoptotic; Bak; Bcl-2; Bcl-XL; cancer; human.

XX OS Homo sapiens.

XX PN WO200302829-A2.

XX PD 31-JUL-2003.

XX PF 17-JAN-2003; 2003WO-GB000165.

XX PR 17-JAN-2002; 2002GB-00000970.

XX PA (UNIV VICTORIA MANCHESTER.

XX PI Griffiths GU;

XX DR WPI; 2003-902664/82.

XX XX Detecting or screening for chemotherapeutic activity, useful for treating

PT cancer, from induction of modifications in Bak protein in cells over

PT expressing anti-apoptotic protein.

XX PS Disclosure; Page 3; 32pp; English.

XX DR WPI; 2004-225572/21.

XX The invention relates to a protein expression enhancing Bcl2 related nucleic acid comprising a first nucleic acid encoding at least one expressible protein and a second nucleic acid encoding at least one Bcl2 related protein, where expression of the expressible protein is enhanced by transcription or translation of the second nucleic acid. The disclosure; SEQ ID NO 6; 43pp; English.

XX The invention relates to a protein expression enhancing Bcl2 related nucleic acid comprising a first nucleic acid encoding at least one expressible protein and a second nucleic acid encoding at least one Bcl2 related protein, where expression of the expressible protein is enhanced by transcription or translation of the second nucleic acid. The disclosure; SEQ ID NO 6; 43pp; English.

CC change in the conformation of cellular Bak, indicative of chemotherapeutic activity, is detected. The anti-apoptotic protein is Bcl-2 or Bcl-XL, and is over expressed by transfecting the cells with a pcDNA3.1 vector that contains the anti-apoptotic-expressing sequence under control of the cytomegalovirus promoter. The method of the invention is used to identify, or screen for, chemotherapeutic agents for the treatment of cancer. The current sequence represents the human Bak amino acid sequence.

XX Sequence 211 AA;

Query Match	Score	DB	Length	AA
Best Local Similarity	100.0%	7	211	
Matches 211; Conservative	100.0%	Pred. No. 1.4e-112		
Mismatches 0; Indels 0; Gaps 0;				
Qy 1 MASCQGPGRPROCGEPALPSASEBQVQAQDTBEVERSYVFYRHQQEAEQVAAPADPEM 60		Db 1 MASCQGPGRPROCGEPALPSASEBQVQAQDTBEVFRSYVFYRHQQEAEQVAAPADPEM 60		
Db 1 MASCQGPGRPROCGEPALPSASEBQVQAQDTBEVFRSYVFYRHQQEAEQVAAPADPEM 60		Qy 61 VTLPLQPSSSTMQGVGRQIAIGDINRYDSFQTMQLQHLOPATAENAYEFTKIASTLFE 120		
Qy 61 VTLPLQPSSSTMQGVGRQIAIGDINRYDSFQTMQLQHLOPATAENAYEFTKIASTLFE 120		Db 61 VTLPLQPSSSTMQGVGRQIAIGDINRYDSFQTMQLQHLOPATAENAYEFTKIASTLFE 120		
Db 61 VTLPLQPSSSTMQGVGRQIAIGDINRYDSFQTMQLQHLOPATAENAYEFTKIASTLFE 120		Qy 121 SGINWGRVVALLGFGYRLAHYQHGQTGFLGQVTRPVUDFMLHHCTARWAQRGWVA 180		
Qy 121 SGINWGRVVALLGFGYRLAHYQHGQTGFLGQVTRPVUDFMLHHCTARWAQRGWVA 180		Db 121 SGINWGRVVALLGFGYRLAHYQHGQTGFLGQVTRPVUDFMLHHCTARWAQRGWVA 180		
Db 121 SGINWGRVVALLGFGYRLAHYQHGQTGFLGQVTRPVUDFMLHHCTARWAQRGWVA 180		Qy 181 LNLTNGNPILNVLVLLGVVLLGQEVVRFFKS 211		
Qy 181 LNLTNGNPILNVLVLLGVVLLGQEVVRFFKS 211		Db 181 LNLTNGNPILNVLVLLGVVLLGQEVVRFFKS 211		
Db 181 LNLTNGNPILNVLVLLGVVLLGQEVVRFFKS 211				

RESULT 11
ID ADL69726 standard; protein; 211 AA.

XX AC ADL69726;

XX DT 20-MAY-2004 (first entry)

XX DB Human Bcl2 related protein #6.

XX BC12 related protein; therapeutic protein; human.
XX OS Homo sapiens.
XX PN US2004043028-A1.

XX XX 04-MAR-2004.

XX XX 02-NOV-2001; 2001US-00003632.

XX PR 02-NOV-2001; 2001US-00003632.

XX XX (LEBC/ LEB C.

XX PA (SHIX/ SHI X.

XX PA (LYCC/ LY C.

XX PA (MOOR/ MOORE G.

XX PI Lee C, Shi X, Ly C, Moore G;

XX XX DR WPI; 2004-225572/21.

XX The invention relates to a protein expression enhancing Bcl2 related nucleic acid comprising a first nucleic acid encoding at least one expressible protein and a second nucleic acid encoding at least one Bcl2 related protein, where expression of the expressible protein is enhanced by transcription or translation of the second nucleic acid. The disclosure; SEQ ID NO 6; 43pp; English.

XX The invention relates to a protein expression enhancing Bcl2 related nucleic acid comprising a first nucleic acid encoding at least one expressible protein and a second nucleic acid encoding at least one Bcl2 related protein, where expression of the expressible protein is enhanced by transcription or translation of the second nucleic acid. The disclosure; SEQ ID NO 6; 43pp; English.

XX The invention relates to a method for detecting a chemotherapeutic activity in a compound other than an etoposide, or in a combination of compounds. In the method of the invention, a cell that over expresses an anti-apoptotic protein is treated with at least one compound, and any

CC anti-apoptotic protein is treated with at least one compound, and any

Db	1	MASGGCGGPPKVGPCKGDES - RPFSEQAQADDEEVRSVYFVLHQEQETQG-RPPANPEM
QY	61	VTLPLQESSTMGQVGROLAISGDINRRYDSEFQMLQHIOPTAENAYEYETKATSLFE 128
Db	58	DNLPLEENSTIUCQVGROLAISGDINRRYDSEFQMLQHIOPTAENAYEYETKATSLFE 111
QY	121	SGINNGRVVALLGGYRLALHYQRLTGFQGVTRPVVDEMHLHCIAIRMAIQRGWVA 188
Db	118	SGISMRVVALLGGYRLALHYQRLTGFQGVTCFLADILHYIARWIAQRGWVA 177
QY	181	LNIGNGPILNLYVGVLLGQFVWRPFKS 211
Db	178	LNLRRPBLITMVIFSVVLLGQFYHRFFRS 208

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Job time : 155 secs

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